

```

PF 19-MAY-1994; 94EP-0303575.
XX
XX 24-MAY-1993; 93US-0068394.
PR 12-AUG-1993; 93US-0106463.
PR 25-AUG-1993; 93US-011758.
PR 03-DEC-1993; 93US-0162407.
PR 07-MAR-1994; 94US-0209502.
PR 11-MAY-1994; 94US-0243345.
XX
XX (IMMUNEX CORP.
XX Beckmann MP, Lyman SD.
XX WPI: 1995-008071/02.
XX N-PSDB: AAQ79079.
XX
XX Isolated ligands for flt 3 receptors - useful for treating
XX anaemia, AIDS and various cancers
XX
XX Disclosure: Page 29-30; 33pp; English.
XX
XX A human T-cell lambda-gli0 random primed cDNA library was
XX screened with a fragment corresponding to the extracellular
XX domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)
XX to isolate human flt3-L cDNA. flt3 stimulates progenitor and
XX stem cells, and can be used e.g. in gene therapy protocols.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 235 AA:
SQ
Query Match 100.0%; Score 1242; DR 16; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
Db 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
QY 61 ASNLDDELGGGLMRVLVAORWMEERLKTVAAGSKMGLERVNTIEHFVTKCAFOPPPSCL 120
Db 61 ASNLDDELGGGLMRVLVAORWMEERLKTVAAGSKMGLERVNTIEHFVTKCAFOPPPSCL 120
QY 121 RFVQNTISRLQETSEDLVALKPMITRONFSRCLQLQCCPDSSSTLPFPWSPRLTATPT 140
Db 121 RFVQNTISRLQETSEDLVALKPMITRONFSRCLQLQCCPDSSSTLPFPWSPRLTATPT 140
QY 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGQVPPVPSPODLLVEH 235
Db 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGQVPPVPSPODLLVEH 235

RESULT 2
AAW67769
ID AAW67769 standard; Protein: 235 AA.
XX
XX AAW67769;
XX
XX 25-MAR-1999 (first entry)
XX
XX Human flt3-ligand.
XX
XX Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
XX immunogenic; autoimmune disease; organ transplantation; food allergy;
XX tissue transplantation.
XX
XX Homo sapiens.
XX
XX MO9857655-A1.
XX
XX 23-DEC-1998.
XX
XX 12-JUN-1998; 98WO-US12085.
XX

```

```

PR 17-JUN-1997; 97US-0877421.
XX
XX (IMMUNEX CORP.
XX Abbott NM, Mowat AM, Viney JL.
XX
XX WPI: 1999-070422/06.
XX N-PSDB: AAV81506.
XX
XX Methods for initiating or enhancing antigen specific immune
XX tolerance - by using murine or human flt3 ligand
XX
XX Claim 1; Page 14-15; 25pp; English.
XX
XX A method has been developed of initiating or enhancing: (i) an antigen-
XX specific immune tolerance; or (ii) immunotolerance of a therapeutic
XX immunogenic molecule by addition of a polypeptide, before, after or with
XX the mucosal administration of an immunotoxin; amount of the antigen
XX or therapeutic molecule, respectively. The polypeptide is capable of
XX binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
XX ligand (flt3-L), where x is an amino acid between 163-231; b) amino
XX acids 28-y of human flt3-L, where y is an amino acid between 160-235;
XX and c) a polypeptide that has at least 90% identity to the polypeptides
XX of either (a) or (b). The method ameliorates the effects of autoimmune
XX diseases, food allergies or organ or tissue rejection following
XX transplantation. Administration of flt3-L allows lower doses of antigens
XX to be used in vivo for mucosally administered antigens. The present
XX sequence represents human flt3-L.
XX
XX Sequence 235 AA:
SQ
Query Match 100.0%; Score 1242; DR 20; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
Db 1 MTVALPAPMSPTTYLLLLSSGLSTGPCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60
QY 61 ASNLDDELGGGLMRVLVAORWMEERLKTVAAGSKMGLERVNTIEHFVTKCAFOPPPSCL 120
Db 61 ASNLDDELGGGLMRVLVAORWMEERLKTVAAGSKMGLERVNTIEHFVTKCAFOPPPSCL 120
QY 121 RFVQNTISRLQETSEDLVALKPMITRONFSRCLQLQCCPDSSSTLPFPWSPRLTATPT 180
Db 121 RFVQNTISRLQETSEDLVALKPMITRONFSRCLQLQCCPDSSSTLPFPWSPRLTATPT 180
QY 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGQVPPVPSPODLLVEH 235
Db 181 APQPPILLLLLPVGLLLAAAMCLHWQRTRRTPRPGQVPPVPSPODLLVEH 235

RESULT 3
AAV69719
ID AAV69719 standard; Protein: 235 AA.
XX
XX AAV69719;
XX
XX 05-JUL-2000 (first entry)
XX
XX Full length wild type human flt-3 protein.
XX
XX Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;
XX neutroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
XX cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
XX cellular expansion; cellular differentiation; natural killer cell;
XX cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
XX myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
XX multiple myeloma; leukemia.
XX
XX Homo sapiens.
XX
XX MO200001823-A2.
XX

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:43:17 : Search time 60.515 Seconds

(without alignments)
616.388 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MYLAPAWMPPTTYJLLLL.....RPGFQVPVPSPQDLLVFR: 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Prd. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1242	100.0	235	16	AA67541 Human flt-3 ligand
2	1242	100.0	235	20	AA67769 Human flt3-ligand
3	1242	100.0	235	21	AA69779 Full length wild t
4	1242	100.0	235	22	AA20192 Human flt-3 ligand
5	1242	100.0	235	23	AA20191 C neofornans anti
6	1242	100.0	235	23	ABG31626 Human flt3l prote
7	1242	100.0	235	23	AB808129 Human flt3l polype
8	1242	100.0	235	24	ABG79949 Secreted human pro
9	1242	100.0	235	24	ABG74239 Human flt-3 ligand

10	1237	99.6	235	24	AA679950 Secreted human pro
11	1236	99.5	235	16	AA66175 Human S66/3109 flt
12	1236	99.5	235	22	AA820194 Human flt-3 ligand
13	1124	90.5	212	21	AA69721 Human flt-3 mutein
14	1114	89.7	209	19	AA669007 Human flt-3 recept
15	1114	89.7	209	21	AA669720 Mature wild type h
16	1110	89.4	209	21	AA669723 Human flt-3 mutein
17	1110	89.4	209	21	AA669726 Human flt-3 mutein
18	1110	89.4	209	21	AA669727 Human flt-3 mutein
19	1110	89.4	209	21	AA669729 Human flt-3 mutein
20	1108	89.2	209	21	AA669722 Human flt-3 mutein
21	1108	89.2	209	21	AA669724 Human flt-3 mutein
22	1107	89.1	209	21	AA669728 Human flt-3 mutein
23	1100	88.6	209	21	AA669725 Human flt-3 ligand
24	970	78.1	185	22	AA620195 Human flt-3 ligand
25	963	77.5	189	24	AA679948 Secreted human pro
26	895.5	72.1	294	21	AA658204 Canine flt-3 ligand
27	894.5	72.0	291	21	AA658210 Canine flt-3 ligand
28	834	67.1	-78	22	AA620193 Canine mature flt-
29	797.5	64.2	268	21	AA658206 Canine flt-3 ligand
30	796.5	64.1	276	21	AA658207 Canine flt-3 ligand
31	791.5	63.7	265	21	AA658211 Canine flt-3 ligand
32	768.5	61.9	231	16	AA667540 Mouse flt-3 ligand
33	768.5	61.9	231	20	AA667688 Murine flt3-ligand
34	768.5	61.9	231	22	AA620186 Mouse flt-3 ligand
35	768.5	61.9	231	24	ABG74238 Mouse flt-3 ligand
36	768	61.8	232	16	AA666177 Mouse flt-3 ligand
37	764	61.5	232	22	AA620189 Mouse flt-3 ligand
38	745	60.0	150	19	AA677930 Flt3 ligand FLT10C
39	745	59.6	150	19	AA669054 Human flt-3 recept
40	740.5	59.6	377	19	AA678124 Chimeric receptor
41	739	59.5	143	19	AA677926 Flt3 ligand FLT3C
42	739	59.5	143	19	AA669050 Human flt-3 recept
43	737.5	59.4	349	19	AA683289 Human flt3 ligand
44	737.5	59.4	349	19	AA678005 Flt3L 1-139/1962b/
45	736.5	59.3	340	19	AA683291 Human flt3 ligand

ALIGNMENTS

RESULT 1	AA67541	standard: Protein: 235 AA.
ID	AA67541	
AC	AA67541	
DT	25-MAR-2003	(updated)
DI	05-AUG-1995	(first entry)
DE	Human flt-3 ligand.	
FW	Human flt-3 ligand: flt3-l; anemia; cancer; AIDS; gene therapy.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Peptide	1..26
FT		/label= Stg-peptide
FT		/note= "signal peptide may extend to position 27"
FT	Domain	27..182
FT		/label= Extracellular-domain
FT		/note= "extracellular domain may start at position 28"
FT	Domain	183..205
FT		/label= Transmembrane-domain
FT		206..235
FT		/label= Cytoplasmic-domain
PN	EP627487-A2.	
XX	07-DEC-1994.	
PD		
XX		

XX	PX	13-JAN-2000.
XX	PD	
PF	25-JUN-1999:	99MO-US14296.
XX	PR	02-JUL-1998: 98US-0109100.
PA	(IMM) IMMUNE CORP.	
PI	Gladis TJ; McGrew JT;	
DR	N-PSDB: AA259064.	
PT	Mutant soluble flt3 ligand polypeptide used in cellular expansion,	
PT	response stimulation or treatment of pathological conditions	
PT	contains amino acid substitutions at positions 8, 84, 118 or 122	
XX		
XX	Claim 1; Page 72-73; 90pp; English.	
CC	The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides	
CC	which exhibits increased or decreased biological activity relative to	
CC	the full length wild type (this sequence) or mature (AAV69720) flt3-L	
CC	polypeptides. The flt3-L protein binds cell surface tyrosine kinase	
CC	receptors and regulate growth and differentiation of hematopoietic	
CC	progenitor cells. The flt3-L protein can be used to induce cellular	
CC	expansion (especially in vivo) or differentiation, e.g. in	
CC	hematopoietic, natural killer (NK) or dendritic cells, especially in the	
CC	presence of growth factors such as interleukins, colony stimulating	
CC	factors or protein kinases. The protein can also modulate, augment or	
CC	enhance a patient's immune response and can be used to treat an immune	
CC	disorder (e.g. allergy, autoimmunity or immunosuppression). The protein	
CC	may be used to treat a pathological condition e.g. myelodysplasia,	
CC	aplastic anemia, HIV infection, breast, small cell lung, testicular or	
CC	ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute	
CC	leukemia.	
XX		
SQ	Sequence 235 AA:	
Query Match	100.0%; Score 1242; DB 21; Length 235;	
Best Local Similarity	100.0%; Pred. NO. 4.9e-109;	
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 MTVLADAWSPPTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDTYLADYPVT	60
DB	1 MTVLADAWSPPTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDTYLADYPVT	60
OY	61 ASNLQDEELGGIMRLVLAQRNRELKTVAASKMGILLLEVNIHFPVKICAPQPSC	120
DB	61 ASNLQDEELGGIMRLVLAQRNRELKTVAASKMGILLERNEIHFPVKICAPQPSC	120
OY	121 RFVQTNISRLLETSFQLVALKPWITTRONFSRCLELCCOPDSSILPPWSPRELENART	180
DB	121 RFVQTNISRLLETSFQLVALKPWITTRONFSRCLELCCOPDSSILPPWSPRELENART	180
OY	181 APQPEPLLLLPLVGLLLLAAMCCHWRTRKRTPRGGEVPPVPSPDILLVFH	235
DB	181 APQPEPLLLLPLVGLLLLAAMCCHWRTRKRTPRGGEVPPVPSPDILLVFH	235
RESULT 4		
ID	AAB20192	
XX	AAB20192 standard; protein: 235 AA.	
XX		
AC	AAB20192:	
DT	14-MAY-2001 (first entry)	
XX		
DE	Human Flt-3 ligand.	
KW	Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;	
KW	immunotherapy; therapy; tumour; cancer; melanoma; glioma;	
KW	lymphoma; autoimmune disease; infection; gene therapy.	

XX	OS	HO	co	sapiens.	
XX	XX	Key	Location/Qualifiers		
XX	XX	Peptide	1..26		
XX	XX	Protein	/label= Signal_peptide		
XX	XX	Domain	27..235		
XX	XX	Domain	/label= Mature_protein		
XX	XX	Domain	27..182		
XX	XX	Domain	/label= Extracellular_domain		
XX	XX	Domain	183..205		
XX	XX	Domain	/label= Transmembrane_domain		
XX	XX	Domain	206..235		
XX	XX	Domain	/label= Cytoplasmic_domain		
XX	XX	MO200109303-A2.			
XX	XX	08-FEB-2001.			
XX	XX	31-JUL-2000; 2000MO-US20679.			
XX	XX	30-JUL-1999; 99US-0146170.			
XX	XX	(VICA-) VICAL INC.			
XX	XX	Hermanson GG;			
XX	XX	WPI: 2001-12319/13.			
XX	XX	N-PSDB: AAF30310.			
XX	XX	Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis)			
XX	XX	Claim 2: Page 132-133; 149pp; English.			
XX	XX	The present sequence is that of human fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, or 27-235 of the ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a phytotherapeutically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceuticals: compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the specification.			
XX	XX	Sequence 235 AA:			
XX	XX	Query Match 100.0%; Score 1242; DB 22; Length 235;			
XX	XX	Best Local Similarity 100.0%; Pred. No. 4.9e-109;			
XX	XX	Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
XX	XX	1 MVLAPAWSPPTTYLLLLLLSSGLSGTODCSFUSHPISSDFAVKIRLSLDYLLDDYPVY 50			
XX	XX	1 MVLAPAWSPPTTYLLLLLLSSGLSGTODCSFUSHPISSDFAVKIRLSLDYLLDDYPVY 50			
XX	XX	61 ASNMODEELCGGLWRLVLAQRMMERLKYAGSKMOGLLELVNTEHFVTKCAFQPPSCL 120			
XX	XX	61 ASNMODEELCGGLWRLVLAQRMMERLKYAGSKMOGLLELVNTEHFVTKCAFQPPSCL 120			

QY 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCCQPPSSITLPPWSPRPLEATAPT 130
Db 121 RFVQTNISRLQETSEQLVAKPWITRONFSRCLQLCCQPPSSITLPPWSPRPLEATAPT 130

QY 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235
Db 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235

RESULT 5

AA019091 standard: Protein; 235 AA.

AA019091;

22-NOV-2002 (first entry)

C neoformans antigen expressing dendritic cell; related protein #1.

Human; fungicide; fungal infection; dendritic cell; antigen;

Cryptococcus neoformans; vaccine; immunostimulant.

Homo sapiens.

WC200266053-A2.

29-AUG-2002.

14-DEC-2001: 2001MO-US48288.

04-JAN-2001: 2001US-259653P.

(IMMV) IMMUNEX CORP.

Thomas EK;

WPI: 2002-674896/72.

Producing a population of activated, Cryptococcus neoformans

antigen-presenting dendritic cells for preventing or treating C.

neoformans infection comprises causing the obtained dendritic cells to

present the antigen -

Disclosure: Page 25-26: 32pp; English.

The present invention relates to a method of producing a population of

activated, Cryptococcus neoformans antigen-presenting dendritic cells,

comprising causing the obtained dendritic cells to present the antigen

and maturing the dendritic cells. The activated, C. neoformans

antigen-expressing dendritic cells are useful for treating, or as

CC vaccines or vaccine adjuvants against, C. neoformans infection, or for

generating antigen-specific T cells. The present sequence is a human

protein shown in the exemplification of the invention.

Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 23; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235
Db 181 APQPLLILLPLVGLLLAAAMCLHMORTRRTRPRGQVPPVPSPODLLLVEH 235

RESULT 6

AG31626 standard: Protein; 235 AA.

AG31626;

29-NOV-2002 (first entry)

Human FLT3L protein.

Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;

dendritic cell maturation agent; T cell enhancing factor; skin cancer;

antigen-specific T cell; prostate cancer; liver cancer; bone tumour;

brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;

actinic keratosis; dendritic cell maturation stimulator; cystostatic;

dendritic cell activator; T cell enhancer; human; FLT3L.

Homo sapiens.

WC200266044-A2.

29-AUG-2002.

23-OCT-2001: 2001MO-US46254.

24-OCT-2000: 2000US-242868P.

(IMMV) IMMUNEX CORP.

Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CK;

WPI: 2002-674891/72.

Treating an individual with tumours or cancers, e.g. liver cancer or

brain tumour, by administering a combination of dendritic cell

populations, T cell enhancing factors and activated, antigen-specific T

cells -

Disclosure: Page 38-39: 44pp; English.

The present invention relates to a new method for treating a tumour -

bearing subject. The method involves administering a combination of 2 to

5 agents comprising dendritic cell mobilisation factor, dendritic cell

maturation agent, tumour-killing agent, T cell enhancing factor or

activated, antigen-specific T cells. The method is useful for treating

CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver

cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or

cervical intraepithelial neoplasia. The present amino acid sequence

represents the human FLT3L protein that was used in the method of the

invention.

Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 23; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 APQPLLILLLLLPVGLLLAAACLMHQRTRRRTRPRGQVPPVPSQDLLVEH 235
 DB 181 APQPLLILLLLLPVGLLLAAACLMHQRTRRRTRPRGQVPPVPSQDLLVEH 235

RESULT 7

ID ABB08129 standard; protein; 235 AA.

AC ABB08129;

DT 10-SEP-2002 (first entry)

DE Human Flt3L polypeptide.

KM Dendritic cell: mobilisation factor; T cell; adjuvant; antibacterial;
 KM fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
 KM tuberculostatic; cytostatic; human; Flt3L.

OS Homo sapiens.

PN WO200236141-A2.

PD 10-MAY-2002.

PE 30-OCT-2001; 2001WO-US44834.

PR 02-NOV-2000; 2000US-245721P.

PA (IMMUNEX CORP.

PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;

PT Thomas EK;

DR WPI; 2002-500114/53.

PT Treating an individual suffering from infection, e.g. inflammation;
 PT chickenpox or AIDS, by administering a combination of dendritic cell
 PT mobilisation factor or maturation agent, T cell enhancing factor and
 PT antigen-specific T cells -

PS Disclosure: Page 37-38; 43pp; English.

CC The invention relates to treating an individual at risk for or suffering
 CC from infection with a pathogenic or opportunistic organism. The method
 CC involves administering a combination of two to five agents comprising:
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 CC or (e) activated, antigen-specific T cells. The methods are useful for
 CC treating an individual at risk for or suffering from infection with a
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 CC (e.g. M. tuberculosis), yeast (e.g. C. albicans) or protozoa (e.g.
 CC T. cruzi, which causes Chaga's disease). The methods are especially
 CC useful for treating an individual suffering from immunosuppression by
 CC enhancing a lymphocyte-mediated immune response. In particular, the
 CC method is useful for treating inflammations, chickenpox, oral or genital
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS,
 CC T cell leukemia or T cell lymphoma. The activated antigen-presenting
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence
 CC represents a human Flt3L polypeptide fragment, that can be used as a
 CC dendritic cell mobilisation factor.

CC Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 23; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGLSGTDCSPFHSPISSDPAVKIRELSDYLLDYPYTV 60
 DB 1 MTVALPAMSPPTTYLLLLLLSSGLSGTDCSPFHSPISSDPAVKIRELSDYLLDYPYTV 60

QY 61 ASNIQDEELCGGLMRVLVAQRMERLKTAVGSKMGLIERVNTETHFVTKCAFQPPPSCL 120
 DB 61 ASNIQDEELCGGLMRVLVAQRMERLKTAVGSKMGLIERVNTETHFVTKCAFQPPPSCL 120

QY 121 RFVQTNISRLQETSEQVALKPMITTRQNFSCLELCQCPDSSSTLPPWSPRPLEATPT 180
 DB 121 RFVQTNISRLQETSEQVALKPMITTRQNFSCLELCQCPDSSSTLPPWSPRPLEATPT 180

QY 181 APQPLLILLLLLPVGLLLAAACLMHQRTRRRTRPRGQVPPVPSQDLLVEH 235
 DB 181 APQPLLILLLLLPVGLLLAAACLMHQRTRRRTRPRGQVPPVPSQDLLVEH 235

RESULT 8

AAG79949

ID AAG79949 standard; protein; 235 AA.

AC AAG79949;

DT 16-MAY-2003 (first entry)

DE Secreted human protein comparison protein #1.

KM Gene: secreted; tyrosine kinase receptor ligand; subfamily:
 KM phosphorylation; kidney; blood; lung; brain glioblastoma; prostate;
 KM colon; leukocyte.

OS Unknown.

PN WO2003002138-A1.

PD 09-JAN-2003.

PE 25-JUN-2002; 2002WO-US20172.

PR 27-JUN-2001; 2001US-0891498.

PA (PEKE) PE CORP NY.

PI Gong F, Ceccardi T, Ladunga I;

PT WPI; 2003-267895/26.

PT New isolated human secreted peptide and nucleic acids, useful for the
 PT development of human therapeutics and diagnostic compositions, drug
 PT screening assays, tissue typing and pharmacogenomic analysis -

PS Disclosure: Fig 2A: 66pp; English.

CC The sequences given in AAG79949-50 are included in the scope of the
 CC invention as they show high levels of similarity to the secreted
 CC peptide of the invention. The secreted protein is related to the
 CC lysosine kinase receptor ligand subfamily. This protein effects
 CC protein phosphorylation. The human secreted peptides are useful in
 CC substantial and specific assays related to functional information of
 CC the peptide sequences, to raise antibodies or to elicit immune response,
 CC as reagents in assays that determine the levels of protein in biological
 CC fluids, and as markers for tissues where the corresponding protein is
 CC expressed. The peptides and the antibodies are useful in drug screening
 CC assays, tissue typing and pharmacogenomic analysis. The nucleic acid
 CC molecules are useful as probes, primers and chemical intermediates in
 CC biological assays, for constructing recombinant vectors, and expressing
 CC antigenic portions of the protein. The peptide and nucleic acid
 CC molecules are useful in the identification of therapeutic proteins and
 CC may serve as models or targets for the development of human therapeutic
 CC agents that modulate human secreted peptide activity in cells and
 CC tissues that express the secreted peptide, such as in kidney, blood,
 CC lung, brain glioblastomas, prostate, colon or leukocytes.

CC Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 24; Length 235;

Best Local Similarity 100.0%; Pred. No. 4.9e-109;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAKIRELSYLLQDYPVY 60
 DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAKIRELSYLLQDYPVY 60
 OY 61 ASNQDEELCGGLRWLYLAQRMERLKTAVGSKKQGLLEHVNTIEHFVTKCAFQPPSCL 120
 DB 61 ASNQDEELCGGLRWLYLAQRMERLKTAVGSKKQGLLEHVNTIEHFVTKCAFQPPSCL 120
 OY 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLQLCCPDSSSTLPPEWSPRELEATPT 180
 DB 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLQLCCPDSSSTLPPEWSPRELEATPT 180
 OY 181 APOPPLLLLLLPVGLLLAAACLIHMQRTRRTPRPGEOVPVPSPQDILLVEH 235
 DB 181 APOPPLLLLLLPVGLLLAAACLIHMQRTRRTPRPGEOVPVPSPQDILLVEH 235

RESULT 9
 ABG74239 standard; Protein: 235 AA.

AC ABG74239:
 DT 16-Apr-2003 (first entry)
 DE Human Flt-3 ligand, Flt-3 L.
 KM Human: flt-3 ligand; flt-3 L; stem cell disorder;
 KM cancer; cytopaenia; myelodysplastic syndrome; gene therapy
 KM refractory anaemia; chronic myelomonocytic leukaemia;
 KM aplastic anaemia; Fanconi's anaemia; pancythaenia; antibody;
 KM bone marrow transplant; cytoreductive therapy; cell expansion;
 KM stem cell mobilisation.
 OS Homo sapiens.
 PN US2002160004-A1.
 PD 31-OCT-2002.
 PF 13-MAR-2002; 2002US-0095449.
 PR 11-MAY-1994; 94US-0243545.
 PR 24-JUN-1996; 96US-069632.
 PR 24-MAY-1993; 93US-0068394.
 PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 19-MAY-1995; 95US-0444632.
 PA (LYMA/) LYMAN S D.
 PA (BECK/) BECKMANN M P.
 PI Lyman SD, Beckmann MP;
 DR MPI: 2003-209211/20.
 DR N-PSDB: ABX16545.
 XX
 PT New antibody binding mouse flt-3 ligand, useful for screening,
 PT diagnostic and biological assays in disorders with elevated serum
 PT levels of flt-3 ligand, such as Fanconi's and myelodysplastic syndrome,
 PT aplastic and refractory anemia -
 PS Example 4; Page 15-16; 18pp; English.
 CC The invention relates to an antibody that binds to mouse flt-3 ligand
 CC (flt-3 L) encoded by the cDNA insert in vector sfHAV-EO410 in Escherichia
 CC coli DH10B cells having American Type Culture Collection (ATCC)
 CC Accession No. 69286, where the ligand comprises the truncated
 CC extracellular domain of mouse flt-3 L. The methods and compositions are

CC useful for screening, diagnostic and biological assays in disorders
 CC having elevated serum levels of flt-3 ligand, such as cancer, cytopaenia,
 CC myelodysplastic syndromes, stem cell disorders, refractory anaemia,
 CC chronic myelomonocytic leukaemia, aplastic anaemia, Fanconi's anaemia
 CC and pancythaenia. Flt-3 L is also useful in allogeneic, syngeneic or
 CC autologous bone marrow transplants in patients undergoing cytoreductive
 CC therapies, as well as cell expansion. Flt-3 L is also useful in gene
 CC therapy and progenitor and stem cell mobilisation systems. The
 CC present sequence represents human flt-3 L.

SQ Sequence 235 AA:
 Query Match 100.0%; Score 1242; DB 24; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.9e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAKIRELSYLLQDYPVY 60
 DB 1 MTVALPAMSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAKIRELSYLLQDYPVY 60
 OY 61 ASNQDEELCGGLRWLYLAQRMERLKTAVGSKKQGLLEHVNTIEHFVTKCAFQPPSCL 120
 DB 61 ASNQDEELCGGLRWLYLAQRMERLKTAVGSKKQGLLEHVNTIEHFVTKCAFQPPSCL 120
 OY 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLQLCCPDSSSTLPPEWSPRELEATPT 180
 DB 121 REVQTNISRLQETSEOLVALKPWITRONFSRCLQLCCPDSSSTLPPEWSPRELEATPT 180
 OY 181 APOPPLLLLLLPVGLLLAAACLIHMQRTRRTPRPGEOVPVPSPQDILLVEH 235
 DB 181 APOPPLLLLLLPVGLLLAAACLIHMQRTRRTPRPGEOVPVPSPQDILLVEH 235

RESULT 10
 AAG79950 standard; Protein: 235 AA.

AC AAG79950:
 DT 16-MAY-2003 (first entry)
 DE Secreted human protein comparison protein #2.
 KM Gene: secreted; tyrosine kinase receptor ligand; subfamily:
 KM phosphorylation; kidney; blood; lung; brain glioblastoma; prostate;
 KM colon; leukocyte.
 OS Unknown.
 PN WO200302138-A1.
 PD 09-JAN-2003.
 PF 25-JUN-2002; 2002WO-0520172.
 PR 27-JUN-2001; 2001US-0891498.
 PA (PEKE) PE CORP NY.
 PI Gong F, Ceccardi T, Ladunga I;
 DR MPI: 2003-267895/26.
 XX
 PT New isolated human secreted peptide and nucleic acids, useful for the
 PT development of human therapeutics and diagnostic compositions, drug
 PT screening assays, tissue typing and pharmacogenomic analysis -
 PS Disclosure; Fig 2B; 66pp; English.
 CC The sequences given in AAG79949-50 are included in the scope of the
 CC invention as they show high levels of similarity to the secreted
 CC peptide of the invention. The secreted protein is related to the
 CC tyrosine kinase receptor ligand subfamily. This protein effects

CC protein phosphorylation. The human secreted peptides are useful in
 CC substantial and specific assays related to functional information of
 CC the peptide sequences, to raise antibodies or to elicit immune response.
 CC as reagents in assays that determine the levels of protein in biological
 CC fluids, and as markers for tissues where the corresponding protein is
 CC expressed. The peptides and the antibodies are useful in drug screening
 CC assays, tissue typing and pharmacogenomic analysis. The nucleic acid
 CC molecules are useful as probes, primers and chemical intermediates in
 CC biological assays, for constructing recombinant vectors, and expressing
 CC antigenic portions of the protein. The peptide and nucleic acid
 CC molecules are useful in the identification of therapeutic proteins and
 CC may serve as models or targets for the development of human therapeutic
 CC agents that modulate human secreted peptide activity in cells and
 CC tissues that express the secreted peptide, such as in kidney, blood,
 CC lung, brain glioblastomas, prostate, colon or leukocytes.

XX Sequence 235 AA:

Query Match 99.6%; Score 1237; DB 24; Length 235;

Best Local Similarity 99.6%; Pred. No. 1.5e-108;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVLAPAMSPPTVYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPVTV 60
 DB 1 MVLAPAMSPPTVYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPVTV 60
 QY 61 ASNLDDELGGIMRLVLAQRMRERLKTAVAGSKMGLLERYNTEIHFVTKCAFQPPPSCL 120
 DB 61 ASNLDDELGGIMRLVLAQRMRERLKTAVAGSKMGLLERYNTEIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180
 QY 181 APOPLLILLPVGLLLAAAMCLHMORTRRRTPRGEOVPPVSPDILLVEH 235
 DB 181 APOPLLILLPVGLLLAAAMCLHMORTRRRTPRGEOVPPVSPDILLVEH 235

RESULT 11

AAR66175

10 AAR66175 standard; Peptide: 235 AA.

XX AAR66175:

XX 25-MAR-2003 (updated)

DT 10-AUG-1995 (first entry)

XX Human S86/S109 Flt3 ligand peptide sequence.

XX Flt3 ligand; tyrosine kinase receptor ligand.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

DR WP1: 1995-096787/01.
 DR N-PSDB; AAQ79642.
 XX New ligand for the Flt3 tyrosine kinase receptor and related
 PT nucleic acid, vectors, host cells and antibodies, useful for
 PT treating abnormal cell physiology and proliferation, e.g. cancer.
 PT also for diagnosis and drug screening

XX Claim 11: Page 76-77; 90pp; English.

CC A cDNA library from the human stromal cell line 293SV40, in
 CC pHEB18, was screened with an 800 bp fragment derived from
 CC mouse clone T118. This fragment encompasses the coding region
 CC conserved between two mouse clones, T18 and T110. Approx. 20
 CC positive clones were selected and partially sequenced. Two
 CC clones, S86 and S109, were found to be approx. 75% homologous
 CC to the mouse clones over the first 163 AAs. Clone S86 continued
 CC to show homology to T110 until the stop codon. Although to a
 CC lesser degree, for an overall homology of 66%. Clones T118 and
 CC S109 do not show homology to each other or to the other clones
 CC after mouse residue 163 (human residue 160). An additional mouse
 CC clone designated M88 has a 29 AA insert at the junction between
 CC the common and divergent portions of the mouse ligand.
 CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 235 AA:

Query Match 99.5%; Score 1236; DB 16; Length 235;

Best Local Similarity 99.6%; Pred. No. 1.8e-108;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVLAPAMSPPTVYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPVTV 60
 DB 1 MVLAPAMSPPTVYLLLLLSGLSGTODCSFQHSPISSDFAVKIRLSDYLLQDPVTV 60
 QY 61 ASNLDDELGGIMRLVLAQRMRERLKTAVAGSKMGLLERYNTEIHFVTKCAFQPPPSCL 120
 DB 61 ASNLDDELGGIMRLVLAQRMRERLKTAVAGSKMGLLERYNTEIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180
 QY 181 APOPLLILLPVGLLLAAAMCLHMORTRRRTPRGEOVPPVSPDILLVEH 235
 DB 181 APOPLLILLPVGLLLAAAMCLHMORTRRRTPRGEOVPPVSPDILLVEH 235

RESULT 12

AAR20194

10 AAR20194 standard; Protein: 235 AA.

XX AAR20194:

XX 14-MAY-2001 (first entry)

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

XX Human Flt-3 ligand.

Key Location/Qualifiers
 FT Peptide /label= Signal-peptide
 FT Protein /label= Mature-protein
 FT Domain /label= Extracellular-domain
 FT Domain /label= Transmembrane-domain

FT Domain 206..235
 FT /label=Cytoplasmic_domain
 XX
 XX WO200109303-A2.
 XX
 XX 08-FEB-2001.
 XX
 XX 31-JUL-2000; 2000WO-US20679.
 XX
 XX 30-JUL-1999; 99US-0146170.
 XX
 XX (VICA-) VICAL INC.
 XX
 XX Hermanson GG;
 XX
 XX WPI: 2001-123319/13.
 DR N-PSDB; AAF30312.
 DR
 PT Immunogenic compositions comprising Flt-3 ligand encoding
 PT polynucleotide and one or more antigen, or cytokine encoding
 PT polynucleotides, useful for suppressing tumour growth and for treating
 PT autoimmune diseases (e.g. rheumatoid arthritis).
 PS
 PS Claim 2; Page 137-138; 149pp: English.
 XX
 CC The present sequence is that of human Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen- or
 CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
 CC polynucleotide may encode the present full-length human Flt-3
 CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235
 CC of the Flt-3 ligand. The polynucleotides are incorporated into
 CC the cells of the vertebrate in vivo, and a prophylactically or
 CC therapeutically effective amount of Flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.
 CC
 XX
 XX
 SO Sequence 235 AA;
 Query Match 99.5%; Score 1236; DB 22; Length 235;
 Best Local Similarity 99.6%; Pred. No. 1.8e-108;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MIVLAPMSPPTTYLLLSGLSGTODCSFOHSPISDFAVKIRELSOYLQDPVTV 60
 DB 1 MIVLAPMSPPTTYLLLSGLSGTODCSFOHSPISDFAVKIRELSOYLQDPVTV 60
 QY 61 ASNLODELCGLRLVLAORWMEKLTAVAGSKMOGLLEPVNTEHFVTKCARQPPSC 120
 DB 61 ASNLODELCGLRLVLAORWMEKLTAVAGSKMOGLLEPVNTEHFVTKCARQPPSC 120
 QY 121 RFVOTNISRLQETSEDIVALKFWITRQNFSCLELOCPDSSSTLPPMSPRLEAVPT 180
 DB 121 RFVOTNISRLQETSEDIVALKFWITRQNFSCLELOCPDSSSTLPPMSPRLEAVPT 180
 QY 181 APQPPILLLLLPVGLLLAAAMCLHMQRTRRRTPRRGEOVPVPSFOLLVEH 235
 DB 181 APQPPILLLLLPVGLLLAAAMCLHMQRTRRRTPRRGEOVPVPSFOLLVEH 235

ID AAF69721 standard; Protein; 212 AA.
 AC AAF69721;
 XX
 XX
 DT 05-JUL-2000 (first entry)
 XX
 XX Human flt-3 mutein L-3H.
 DE
 XX
 KM Immunomodulator; immunosuppressive; cytostatic; anti-HIV;
 KM neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergic;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia; mutein.
 XX
 XX Homo sapiens.
 OS
 CS Synthetic.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 EF
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMNV) IMVUNEX CORP.
 XX
 PT Gradalis J; McGrew JT;
 XX
 DR WPI: 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 XX Claim 4; Page 79-80; 90pp: English.
 PS
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AA69719) or mature (AA69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt3-L
 CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 CC
 XX
 XX
 SO Sequence 212 AA;
 Query Match 90.5%; Score 1124; DB 21; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.9e-99;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 SGTODCSFOHSPISDFAVKIRELSOYLQDPVTVASNIQDELGGLRLVLAORWME 84
 DB 2 SGTODCSFOHSPISDFAVKIRELSOYLQDPVTVASNIQDELGGLRLVLAORWME 84
 QY 85 RIKTVAGSKMOGLLEPVNTEHFVTKCARQPPSCIRFVOTNISRLQETSEDIVALKFW 144
 DB 62 RIKTVAGSKMOGLLEPVNTEHFVTKCARQPPSCIRFVOTNISRLQETSEDIVALKFW 121
 QY 145 TTRQNFSCLELOCPDSSSTLPPMSPRLEAVPTAPQPPILLLLLPVGLLLAAAMC 204

QY	27	TQPCSCQHSPISSDPAVKIRELSIDLDDY:VTASNSIQDEELCCGRLVLAQRMERL	86
Db	1	TQPCSCQHSPISSDPAVKIRELSIDLDDY:VTASNSIQDEELCCGRLVLAQRMERL	60
QY	87	KTVASCKMGILLERNVTEIHFTKCAFOPPSCILFVYQTNISRLLOETSPQVLAKMIT	148
Db	61	KTVASCKMGILLERNVTEIHFTKCAFOPPSCILFVYQTNISRLLOETSPQVLAKMIT	120
QY	147	RONFSSCLFLQCCPDSTILFPWSPRPIEATAP--APQPELLLLLLPYGDLILAAACLI	206
Db	121	RONFSCLELQCCPDSTILFPWSPRPIEATAPAPQPELLLLLLPYGDLILAAACLI	187
QY	267	WQTRRRTRPRGQVPPVPSPDLLVNH 235	
Db	181	WQTRRRTRPRGQVPPVPSPDLLVNH 209	
RESULT 15			
ID	AAV69720	standard; Protein; 209 AA.	
XX	AAV69720:		
AC	05-JUL-2000	(first entry)	
CT			
XX			
DE		Mature wild type human flt-3 protein.	
XX			
KM		Immunomodulator; immunosuppressive; cytostatic; antitumoric; anti-HIV;	
KM		neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;	
KM		cell surface tyrosine kinase receptor; hematopoietic progenitor cell;	
KM		cellular expansion; cellular differentiation; natural killer cell;	
KM		cancer; dendritic cell; immune response; autoimmunity; immunosuppression;	
KM		myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;	
XX		multiple myeloma; leukemia.	
OS		Homo sapiens.	
XX			
PN	W0200001823-A2.		
XX			
FD	13-JAN-2000.		
XX			
FP	25-JUN-1999;	99MO-US14296.	
XX			
PR	02-JUL-1998;	98US-0109100.	
XX			
PA	(IMMUNEX CORP.		
XX			
XX	Graddis TJ, McGrew JT;		
DR	WPI: 2000-182115/16.		
DR	N-PSDB: AA259064.		
XX			
FT		Mutant soluble flt3 ligand polypeptide used in cellular expansion,	
FT		immune response stimulation or treatment of pathological conditions	
XX		contains amino acid substitutions at positions 8, 84, 118 or 122	
PS	Claim 1: Page 89-90; 90pp: English.		

CC leukemia.
XX
SQ Sequence 209 AA;

Query Match 89.7%; Score 1114; DB 21; Length 209;
Best Local Similarity 100.0%; Pred. No. 5,1e-97;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 27 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVASNIQDEELCGGLMRLYLAQRMERL 86
   |||
Db 1 TODCSFOHSPISSDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLMRLYLAQRMERL 60
   |||

QY 87 KTVAGSKMGLERVNTETHFVTKCAFQPPSCIRFYQTNISRLQETSEQLVALKPWIT 146
   |||
Db 61 KTVAGSKMGLERVNTETHFVTKCAFQPPSCIRFYQTNISRLQETSEQLVALKPWIT 120
   |||

QY 147 RQNFSCLELQCPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLLPVGLLLAAACLI 206
   |||
Db 121 RQNFSCLELQCPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLLPVGLLLAAACLI 180
   |||

QY 207 MORTRRTRPRGEOYPPVPSPODLLVEH 235
   |||
Db 181 MORTRRTRPRGEOYPPVPSPODLLVEH 203
   |||
```

Search completed: September 15, 2003, 15:54:23
Job time : 61.515 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 15, 2003, 15:52:22 : Search time 20.676 Seconds
(without alignments)
480.899 Million cell updates/sec

Title: US-09-448-378-1
Perfect score: 1242
Sequence: 1 MVLAPAWSPRTYLLILL.....PGEQVVPVSPQDLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
5: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfillsi.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1	US-08-243-545-6 Sequence 6, Appl.
2	1242	100.0	235	2	US-08-993-962-6 Sequence 6, Appl.
3	1242	100.0	235	3	US-09-160-841-6 Sequence 6, Appl.
4	1242	100.0	235	3	US-09-109-100-1 Sequence 6, Appl.
5	1242	100.0	235	5	PCT-US94-05365-5 Sequence 6, Appl.
6	1124	90.5	212	3	US-09-109-100-10 Sequence 18, Appl.
7	1114	89.7	209	3	US-09-109-100-18 Sequence 18, Appl.
8	1110	89.4	209	3	US-09-109-100-9 Sequence 9, Appl.
9	1110	89.4	209	3	US-09-109-100-12 Sequence 12, Appl.
10	1110	89.4	209	3	US-09-109-100-14 Sequence 14, Appl.
11	1110	89.4	209	3	US-09-109-100-11 Sequence 17, Appl.
12	1108	89.2	209	3	US-09-109-100-11 Sequence 11, Appl.
13	1108	89.1	209	3	US-09-109-100-15 Sequence 13, Appl.
14	1107	89.1	209	3	US-09-109-100-13 Sequence 13, Appl.
15	1106	89.0	209	3	US-09-109-100-8 Sequence 8, Appl.
16	1100	88.6	209	3	US-09-109-100-16 Sequence 16, Appl.
17	895.5	72.1	234	4	US-09-322-409-7 Sequence 7, Appl.
18	895.5	72.1	234	4	US-09-451-527-7 Sequence 7, Appl.
19	894.5	72.0	231	4	US-09-322-409-44 Sequence 44, Appl.
20	894.5	72.0	231	4	US-09-451-527-44 Sequence 44, Appl.
21	797.5	64.2	268	4	US-09-322-409-23 Sequence 23, Appl.
22	797.5	64.2	268	4	US-09-451-527-23 Sequence 23, Appl.
23	796.5	64.1	276	4	US-09-322-409-26 Sequence 26, Appl.
24	796.5	64.1	276	4	US-09-451-527-26 Sequence 26, Appl.
25	791.5	63.7	265	4	US-09-322-409-49 Sequence 49, Appl.
26	791.5	63.7	265	4	US-09-451-527-49 Sequence 49, Appl.
27	768.5	61.9	231	1	US-08-243-545-2 Sequence 2, Appl.

28	768.5	61.9	231	2	US-08-993-962-2	Sequence 2, Appl.
29	768.5	61.9	231	3	US-09-160-841-2	Sequence 2, Appl.
30	768.5	61.9	231	5	PCT-US94-05365-2	Sequence 2, Appl.
31	765.5	61.6	231	1	US-08-220-3798-7	Sequence 7, Appl.
32	765.5	61.6	231	5	PCT-US95-03866-6	Sequence 6, Appl.
33	698.5	56.2	250	4	US-09-322-409-31	Sequence 31, Appl.
34	698.5	56.2	250	4	US-09-451-527-31	Sequence 31, Appl.
35	506.5	40.8	137	3	US-09-109-100-19	Sequence 19, Appl.
36	154	12.4	42	5	PCT-US94-05350-17	Sequence 17, Appl.
37	91.5	7.4	673	1	US-08-317-522A-9	Sequence 9, Appl.
38	91.5	7.4	673	1	US-08-439-8-8A-9	Sequence 9, Appl.
39	91.5	7.4	673	2	US-08-751-965-9	Sequence 9, Appl.
40	91.5	7.4	673	2	US-08-738-975-9	Sequence 9, Appl.
41	91.5	7.4	673	2	US-08-728-626-9	Sequence 9, Appl.
42	91.5	7.4	673	3	US-08-808-559A-9	Sequence 9, Appl.
43	89.5	7.2	941	4	US-09-390-134B-31	Sequence 31, Appl.
44	87.5	7.0	415	3	US-09-006-353A-6	Sequence 6, Appl.
45	87.5	7.0	415	4	US-09-573-966-6	Sequence 6, Appl.

ALIGNMENTS

RESULT :
US-08-243-545-6
Sequence 6, Application US/08243545
Patent No. 5594512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flk3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
Z-IP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%: Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%: Pred. No. 2,3e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPISDFAVKIRLSYLLQYEVTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPISDFAVKIRLSYLLQYEVTV 60
QY 61 ASNLODELCGJLWVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
DB 61 ASNLODELCGJLWVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQVIAKPMITRONFSRCLELCCQPDSSSTLPPWSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQVIAKPMITRONFSRCLELCCQPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLLLLLPVGLLLAAAWCLHMQRTRRPRPGEOVPPVPSQDILLVH 235
DB 181 APQPLLLLLLPVGLLLAAAWCLHMQRTRRPRPGEOVPPVPSQDILLVH 235

RESULT 2
US-08-993-962-6
Sequence 6, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for fli3/fik-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%: Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%: Pred. No. 2,3e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPISDFAVKIRLSYLLQYEVTV 60
DB 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQSPISDFAVKIRLSYLLQYEVTV 60
QY 61 ASNLODELCGJLWVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
DB 61 ASNLODELCGJLWVLAQRMERLKTVAASKMOGLLEEVNTLEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQVIAKPMITRONFSRCLELCCQPDSSSTLPPWSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQVIAKPMITRONFSRCLELCCQPDSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLLLLLPVGLLLAAAWCLHMQRTRRPRPGEOVPPVPSQDILLVH 235
DB 181 APQPLLLLLLPVGLLLAAAWCLHMQRTRRPRPGEOVPPVPSQDILLVH 235

RESULT 3
US-09-160-841-5
Sequence 6, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for fli3/fik-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:57:23 ; Search time 40.3433 Seconds
(without alignments)
849.940 Million cell updates/sec

Title: US-09-448-378-1
Perfect score: 1242
Sequence: 1 MVLAPAWSPFTYLLLL.....RPEGEQVPVPSPQDLLEVRH 235

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications, AA:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	7 US-08-994-468-6	Sequence 5, Appl
2	1242	100.0	235	9 US-09-448-378-1	Sequence 1, Appl
3	1242	100.0	235	10 US-09-983-806-6	Sequence 6, Appl
4	1242	100.0	235	10 US-09-904-536-1	Sequence 1, Appl
5	1242	100.0	235	12 US-10-314-035-6	Sequence 6, Appl
6	1242	100.0	235	14 US-10-095-449-6	Sequence 6, Appl
7	1242	100.0	235	15 US-10-241-927-2	Sequence 2, Appl
8	1124	90.5	212	10 US-09-904-536-10	Sequence 18, Appl
9	1114	89.7	209	10 US-09-904-536-9	Sequence 9, Appl
10	1110	89.4	209	10 US-09-904-536-12	Sequence 12, Appl
11	1110	89.4	209	10 US-09-904-536-14	Sequence 14, Appl
12	1110	89.4	209	10 US-09-904-536-17	Sequence 11, Appl
13	1108	89.2	209	10 US-09-904-536-11	Sequence 15, Appl
14	1108	89.2	209	10 US-09-904-536-15	Sequence 15, Appl

16	1107	89.1	209	10	US-09-904-536-13	Sequence 13, Appl
17	1106	89.0	209	10 <th>US-09-904-536-8</th> <th>Sequence 8, Appl</th>	US-09-904-536-8	Sequence 8, Appl
18	1100	88.6	209	10 <th>US-09-904-536-16</th> <th>Sequence 16, Appl</th>	US-09-904-536-16	Sequence 16, Appl
19	895.5	72.1	294	12 <th>US-10-262-439-7</th> <th>Sequence 7, Appl</th>	US-10-262-439-7	Sequence 7, Appl
20	895.5	72.1	294	15 <th>US-10-218-654-7</th> <th>Sequence 7, Appl</th>	US-10-218-654-7	Sequence 7, Appl
21	894.5	72.0	291	12 <th>US-10-262-439-44</th> <th>Sequence 44, Appl</th>	US-10-262-439-44	Sequence 44, Appl
22	894.5	72.0	291	15 <th>US-10-218-654-44</th> <th>Sequence 44, Appl</th>	US-10-218-654-44	Sequence 44, Appl
23	882	66.2	156	15 <th>US-10-051-355A-1</th> <th>Sequence 1, Appl</th>	US-10-051-355A-1	Sequence 1, Appl
24	797.5	64.2	268	12 <th>US-10-262-439-23</th> <th>Sequence 23, Appl</th>	US-10-262-439-23	Sequence 23, Appl
25	797.5	64.2	268	12 <th>US-10-218-654-23</th> <th>Sequence 23, Appl</th>	US-10-218-654-23	Sequence 23, Appl
26	796.5	64.1	276	15 <th>US-10-262-439-26</th> <th>Sequence 26, Appl</th>	US-10-262-439-26	Sequence 26, Appl
27	796.5	64.1	276	15 <th>US-10-218-654-26</th> <th>Sequence 26, Appl</th>	US-10-218-654-26	Sequence 26, Appl
28	791.5	63.7	265	12 <th>US-10-262-439-49</th> <th>Sequence 49, Appl</th>	US-10-262-439-49	Sequence 49, Appl
29	791.5	63.7	265	15 <th>US-10-218-654-49</th> <th>Sequence 49, Appl</th>	US-10-218-654-49	Sequence 49, Appl
30	768.5	61.9	231	7 <th>US-08-994-468-2</th> <th>Sequence 2, Appl</th>	US-08-994-468-2	Sequence 2, Appl
31	768.5	61.9	231	9 <th>US-09-448-378-2</th> <th>Sequence 2, Appl</th>	US-09-448-378-2	Sequence 2, Appl
32	768.5	61.9	231	10 <th>US-09-983-806-2</th> <th>Sequence 2, Appl</th>	US-09-983-806-2	Sequence 2, Appl
33	768.5	61.9	231	12 <th>US-10-314-035-2</th> <th>Sequence 2, Appl</th>	US-10-314-035-2	Sequence 2, Appl
34	768.5	61.9	231	14 <th>US-10-095-449-2</th> <th>Sequence 2, Appl</th>	US-10-095-449-2	Sequence 2, Appl
35	698.5	56.2	250	12 <th>US-10-262-439-31</th> <th>Sequence 31, Appl</th>	US-10-262-439-31	Sequence 31, Appl
36	698.5	56.2	250	15 <th>US-10-218-654-31</th> <th>Sequence 31, Appl</th>	US-10-218-654-31	Sequence 31, Appl
37	506.5	40.8	137	10 <th>US-09-904-536-19</th> <th>Sequence 19, Appl</th>	US-09-904-536-19	Sequence 19, Appl
38	97.5	7.9	658	12 <th>US-10-304-946-14</th> <th>Sequence 14, Appl</th>	US-10-304-946-14	Sequence 14, Appl
39	91.5	7.4	674	10 <th>US-09-899-471-2</th> <th>Sequence 2, Appl</th>	US-09-899-471-2	Sequence 2, Appl
40	91.5	7.4	698	10 <th>US-09-899-471-5</th> <th>Sequence 5, Appl</th>	US-09-899-471-5	Sequence 5, Appl
41	91.5	7.4	698	11 <th>US-09-866-050A-509</th> <th>Sequence 509, Appl</th>	US-09-866-050A-509	Sequence 509, Appl
42	91.5	7.4	698	11 <th>US-09-863-818A-8</th> <th>Sequence 8, Appl</th>	US-09-863-818A-8	Sequence 8, Appl
43	89.5	7.2	874	9 <th>US-09-826-509-26</th> <th>Sequence 26, Appl</th>	US-09-826-509-26	Sequence 26, Appl
44	89.5	7.2	941	9 <th>US-09-818-879-47</th> <th>Sequence 47, Appl</th>	US-09-818-879-47	Sequence 47, Appl
45	89.5	7.2	941	9 <th>US-09-211-755B-47</th> <th>Sequence 47, Appl</th>	US-09-211-755B-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-994-468-6
Sequence 6, Application US/08994468
Publication No. US20030148516A1
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for IL13/ILK-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,468
FILING DATE: 19-Dec-1997
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: <unknown>
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430
TELEEX: (206) 233-0644

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids
TYPE: amino acid

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-994-468-6

Query Match 100.0%; Score 1242; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.7e-103;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

DB 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

QY 121 REVQTNISRLQETSEDLVAKPWITRONFSKCLELQCPDSSSTLPPWSPRPLEATAFT 180

DB 121 REVQTNISRLQETSEDLVAKPWITRONFSKCLELQCPDSSSTLPPWSPRPLEATAFT 180

QY 181 AQPPLLILLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPSODLLLVEN 235

DB 181 AQPPLLILLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPSODLLLVEN 235

RESULT 2

US-09-448-378-1

Sequence 1: Application US/09448378
Patent No. US20020034517A1

GENERAL INFORMATION:
APPLICANT: Bristol, Kenneth

TITLE OF INVENTION: Dendritic Cell Stimulatory Factor

FILE REFERENCE: 2836-D

CURRENT APPLICATION NUMBER: US/09/448,378

CURRENT FILING DATE: 1999-11-23

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 1

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

US-09-448-378-1

Query Match 100.0%; Score 1242; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.7e-103;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

DB 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

QY 121 REVQTNISRLQETSEDLVAKPWITRONFSKCLELQCPDSSSTLPPWSPRPLEATAFT 180

DB 121 REVQTNISRLQETSEDLVAKPWITRONFSKCLELQCPDSSSTLPPWSPRPLEATAFT 180

QY 181 AQPPLLILLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPSODLLLVEN 235

DB 181 AQPPLLILLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPSODLLLVEN 235

RESULT 3

US-09-983-806-6
Sequence 6: Application US/09983806
Patent No. US20020107365A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for IL13/IL13 Receptors
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSER: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street
CITY: Seattle

STATE: Washington
COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version 5.1

CURRENT APPLICATION DATA:
FILING DATE: US/09/983,806

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/444,626
FILING DATE: 19-MAY-1995

APPLICATION NUMBER: US 08/762,407
FILING DATE: 03-DEC-1993

APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.7e-103;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

DB 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60

QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTVAAGSKMGLERVNTETHEFTKCAFOPPPSCL 120

QY 121 REVQTNISRLQETSEDLVAKPWITRONFSKCLELQCPDSSSTLPPWSPRPLEATAFT 180

DB 121 REVQTNISRLQETSEDLVAKPWITRONFSKCLELQCPDSSSTLPPWSPRPLEATAFT 180

QY 181 AQPPLLILLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPSODLLLVEN 235

DB 181 AQPPLLILLLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPSODLLLVEN 235

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:52:07 : Search time 25.7189 Seconds
(without alignments)
878.718 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MVLAPAMSPFTYLLLLLL.....RPGEQVPVPSPQDLLLVEN 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	2 I38440	flt3 ligand - huma
2	864.5	69.6	245	2 S43293	FLT3/FLK2 ligand (
3	834	67.1	178	2 I39076	FLT3 ligand altero
4	768.5	61.9	231	2 A45265	FLT3/FLK2 ligand (
5	606.5	48.8	220	2 S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	2 I58343	FLT3 ligand isofor
7	93	7.5	1217	2 T2672	hypothetical prote
8	92	7.4	661	1 TMBE12	74k alpha trans-in
9	89.5	7.2	474	2 T19543	hypothetical prote
10	89	7.2	387	2 I18201	hypothetical prote
11	89	7.2	793	1 S60735	adhalin - goldee b
12	88.5	7.1	238	2 A11990	splicing factor SF
13	88.5	7.1	1386	2 T00257	hypothetical prote
14	88	7.1	753	2 J00532	hypothetical prote
15	87.5	7.0	479	1 A32290	CP protein - Keene
16	87	7.0	910	2 A53137	protein-lysine-rf
17	86.5	7.0	590	2 A40437	tyrosine kinase-rf
18	86	6.9	299	2 T17832	glutamic acid-rich
19	86	6.9	485	2 A33647	hypothetical prote
20	86	6.9	746	2 T28004	sulfated surface p
21	85	6.8	289	2 A67646	hypothetical prote
22	85	6.8	366	2 A37374	hypothetical prote
23	84	6.8	263	2 T03162	PC gamma (Igf) rec
24	84	6.8	757	2 A39283	tegment protein: 6
25	83.5	6.7	199	2 E75630	gamma-glutamyl car
26	83.5	6.7	530	2 A45690	hypothetical prote
27	83	6.7	1509	2 T19486	transactivator E3N
28	82.5	6.6	418	2 T19800	hypothetical prote
29	82.5	6.6	426	2 I36948	hypothetical prote

30	82.5	6.6	512	2 D40829	activin receptor 1
31	82.5	6.6	513	2 J01484	activin receptor P
32	82	6.6	106	2 T06479	proline/leucine-ri
33	82	6.6	854	2 T23837	hypothetical prote
34	81.5	6.6	485	2 C75460	hypothetical prote
35	81.5	6.6	488	2 S13423	stromelysin 3 (EC
36	81.5	6.6	958	2 T13593	hypothetical prote
37	81.5	6.6	1119	2 T50995	related to cytoske
38	81	6.5	156	2 B48232	cysteine-rich exte
39	81	6.5	209	2 A48232	cysteine-rich exte
40	81	6.5	294	2 A12016	hypothetical prote
41	81	6.5	388	2 S15591	probable transposa
42	81	6.5	428	1 FHHU	Ig epsilon chain C
43	80.5	6.5	636	2 J00047	class I cytol kinase
44	80.5	6.5	1376	2 T49482	hypothetical prote
45	80.5	6.5	1306	2 T13592	hypothetical prote

ALIGNMENTS

RESULT: 1	
I38440	flt3 ligand - human
C:Species: Homo sapiens (man)	
C:Date: 29-May-1998	*sequence-revision 29-May-1998 *text-change 01-Dec-2000
C:Accession: I38440; 139075; S43292	
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe	
Blood 83, 2795-2801, 1994	
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor for	
A:Reference number: I38440; M0ID:94235842; PMID:8180375	
A:Accession: I38440	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1235 <RES>	
A:Cross-references: EMBL:U03858; NID:q494978; PIDD:AAA19825.1; PID:q494979	
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.	
Oncogene 11, 1165-1172, 1995	
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.	
A:Reference number: 139075; M0ID:96032581; PMID:7566977	
A:Accession: 139075	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: DNA	
A:Residues: 1-235 <RES>	
A:Cross-references: EMBL:U03874; NID:q1072036; PIDD:AAA90949.1; PID:q1072037	
R:Hannum, C.; Cupepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;	
Teitel, A.; Muench, M.; Kelnier, G.; Nankawa, K.; Reznick, D.; Roncarolo, M.G.; Zlotnik	
Nature 366, 643-648, 1994	
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoie	
A:Reference number: S43290; M0ID:94195428; PMID:8145851	
A:Accession: S43292	
A>Status: preliminary	
A:Molecule type: mRNA	
A:Residues: 1-71, 'A', '73'-235 <HAN>	
A:Cross-references: GB:U04805; NID:q483844; PIDD:AAA17599.1; PID:q483845	
A>Note: the authors translated the codon AGT for residue 25 as Met	
C:Genetics:	
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 226/3	
Query Match	100.0%; Score 1242; DB 2; Length 235;
Best local similarity	100.0%; Pred. No. 5, 1e-93;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MVLAPAMSPFTYLLLLLLSSGLSGTQDSFQHSPISSDFAAVIRELSDYLLQDYPPVTV 60
DB	1 MVLAPAMSPFTYLLLLLLSSGLSGTQDSFQHSPISSDFAAVIRELSDYLLQDYPPVTV 60
QY	61 ASNIDDEUCGCGIRLVLAARMRERLKTVAGSKMGCLLENVNIHFVTKCAQPPSPSCL 120
DB	61 ASNIDDEUCGCGIRLVLAARMRERLKTVAGSKMGCLLENVNIHFVTKCAQPPSPSCL 120
QY	121 RFOVNTSPILQESDEQVLAQKPIRPNFSPKLETLQCGQDSSTLPWPSPRPLETAAPT 180
DB	121 RFOVNTSPILQESDEQVLAQKPIRPNFSPKLETLQCGQDSSTLPWPSPRPLETAAPT 180

Db 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSSTLPPWSPPELEATAP 180

QY 181 APQPLLILLLPVGLLLLAAMCLMORTRRTPRPGQVPPVPSPODLLVEH 235

Db 181 APQPLLILLLPVGLLLLAAMCLMORTRRTPRPGQVPPVPSPODLLVEH 235

RESULT 2

S43293

FLT3/FLK2 ligand (clone S109) - human

C:Species: Homo sapiens (man)

C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1993

C:Accession: S43293

R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kofelt, A.; Muench, M.; Kelnier, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A

Nature 368, 643-648, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43293

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-245 <HAN>

A:Note: the authors translated the codon AGT for residue 25 as Met

Query Match: 69.6%; Score 864.5; DB 2; Length 245;

Best Local Similarity 73.0%; Pred. No. 11e-66;

Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60

Db 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60

QY 61 ASNLQDEELCGGLRWLVLAQRMERLKTVAAGSKMOGLLEKRVNTEHFVTKCAFQPPSPSC 120

Db 61 ASNLQDEELCGGLRWLVLAQRMERLKTVAAGSKMOGLLEKRVNTEHFVTKCAFQPPSPSC 120

QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSSTLPPWSPPELEATAP 160

Db 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSSTLPPWSPPELEATAP 160

QY 181 APQPLLILLLPVGLLLLAAMCLMORTRRTPRPGQVPPVPSPODLLVEH 235

Db 178 WPRPHGEDTEAHRGESP-----ARCGIATWTKRKLARGSLIPWAPLIPSP 222

QY 228 Q 228

Db 223 E 223

RESULT 3

FLT3 ligand alternatively spliced isoform - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I39076

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581; PMID:7566577

A:Accession: I39076

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-178 <RES>

A:Cross-references: EMBL:U29874; NID:g1072036; P1DN:AAA90950.1; P1D:g1072034

C:Genetics: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 3.2e-64;

Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 60

QY 61 ASNLQDEELCGGLRWLVLAQRMERLKTVAAGSKMOGLLEKRVNTEHFVTKCAFQPPSPSC 120

Db 61 ASNLQDEELCGGLRWLVLAQRMERLKTVAAGSKMOGLLEKRVNTEHFVTKCAFQPPSPSC 120

QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSSTLPPWSPPELEATAP 160

Db 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSSTLPPWSPPELEATAP 160

RESULT 4

A49265

FLT3/FLK-2 ligand precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C:Accession: A49265; I49347; I49346; S43290

R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl

D.; Williams, D.E.; Beckman, M.P.

Cell 75, 1157-1167, 1993

A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a

A:Reference number: A49265; MUID:94084751; PMID:7505204

A:Accession: A49265

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-231 <LYM>

A:Cross-references: EMBL:U29875; NID:g1072039; P1DN:AAA94346.1; P1D:g439442

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581; PMID:7566577

A:Accession: I49347

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-163; 'G', '165', 'HYAG' <RES>

A:Cross-references: EMBL:U29875; NID:g1072039; P1DN:AAA90952.1; P1D:g1072041

A:Accession: I49346

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197; 'L', '198-231' <RE2>

A:Cross-references: EMBL:U29875; NID:g1072039; P1DN:AAA90951.1; P1D:g1072040

R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Felt, A.; Muench, M.; Kelnier, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik

Nature 368, 643-648, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43290

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197; 'L', '198-231' <HAN>

A:Experimental source: clone 1110

A:Note: The sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-

C:Genetics: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3

C:Keywords: transmembrane protein

Query Match 61.9%; Score 768.5; DB 2; Length 231;

Best Local Similarity 70.3%; Pred. No. 1.7e-56;

Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 59

Db 1 MYVLAPAMSPPTTYLLLLSSGLSTQDCSFQHSPISSDFAVKIRELSDYLLQDPVTV 59

QY 61 ASNLQDEELCGGLRWLVLAQRMERLKTVAAGSKMOGLLEKRVNTEHFVTKCAFQPPSPSC 119

Db 61 ASNLQDEELCGGLRWLVLAQRMERLKTVAAGSKMOGLLEKRVNTEHFVTKCAFQPPSPSC 120

QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSSTLPPWSPPELEATAP 177

Db 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELQCPDSSSTLPPWSPPELEATAP 180

QY 178 APTAPPP--LTLILLLPVGLLLLAAMCLMORTRRTPRPGQVPPVPSPODLLVEH 227

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:44:07 ; Search time 14.1202 seconds
(without alignments)
782.659 Million cell updates/sec

Title: US-09-448-378-1
Perfect score: 1242
Sequence: 1 MYLAPAWSPFTYLLLLLL.....RPGGVPPVSPDLLLVEN 235

Scoring table: BLOSUM62
Gap: 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 FLJ3L_HUMAN	P49771 homo sapien
2	768	61.8	232	1 FLJ3L_MOUSE	P49772 mus musculu
3	92	7.4	661	1 AT12_VZVD	P09264 varicella-z
4	90.5	7.3	5120	1 PCLO_CHICK	Q9PU36 gallus gall
5	89.5	7.2	941	1 GBR2_HUMAN	Q75899 homo sapien
6	89	7.2	387	1 SGCA_MESAU	Q64255 mesocricetu
7	89	7.2	793	1 S3A1_HUMAN	Q15459 homo sapien
8	87.5	7.0	415	1 INR3_MOUSE	P50284 mus musculu
9	87.5	7.0	479	1 MPR-DROME	P20483 drosophila
10	87	7.0	910	1 DDRI1_MOUSE	Q63474 rattus norv
11	87	7.0	911	1 DDRI1_MOUSE	Q63475 mus musculu
12	86.5	7.0	1394	1 NGC4_BOVIN	Q28181 bos taurus
13	86	6.9	485	1 SSGP_VOLCA	P21997 volvox carl
14	85	6.8	282	1 ATFS_HUMAN	Q95289 homo sapien
15	85	6.8	366	1 FCCN_RAT	P13599 rattus norv
16	84.5	6.8	3726	1 ABF1_MOUSE	Q61359 mus musculu
17	84	6.8	592	1 MNT_HUMAN	Q95563 homo sapien
18	84	6.8	732	1 E4L5_HUMAN	Q95563 homo sapien
19	84	6.8	1234	1 NPHN_RAT	Q91044 rattus norv
20	83.5	6.7	671	1 2282_HUMAN	Q94047 homo sapien
21	83	6.7	756	1 VKGC_HUMAN	P38435 homo sapien
22	82.5	6.6	334	1 BC12_HUMAN	Q94047 homo sapien
23	82	6.6	2167	1 SHK1_RAT	Q94047 rattus norv
24	81.5	6.6	488	1 MM11_HUMAN	P24378 mus musculu
25	81.5	6.6	591	1 MNT_MOUSE	Q08789 mus musculu
26	81.5	6.6	2212	1 T230_HUMAN	Q93074 homo sapien
27	81	6.5	283	1 ATFS_MOUSE	Q70191 mus musculu
28	81	6.5	387	1 SGCA_MOUSE	P23350 mus musculu
29	81	6.5	428	1 EPC_HUMAN	P01854 homo sapien
30	81	6.5	1248	1 DIAT_HUMAN	Q60610 homo sapien
31	80.5	6.5	1402	1 IF4G_RABIT	P11110 oryctolagus
32	80	6.4	397	1 CEFD_STRL	P18549 streptomyces
33	80	6.4	940	1 GBR2_RAT	Q68871 rattus norv

34	80	6.4	1174	1 KPC1_COCHF	Q42632 cochllobolus
35	80	6.4	1427	1 ZFH2_HUMAN	Q96041 homo sapien
36	80	6.4	1794	1 YDC9_SCHPO	Q10172 schizosacch
37	79.5	6.4	5085	1 PCLO_RAT	Q93K56 rattus norv
38	79	6.4	805	1 KIP3_YEAST	P53086 saccharomyces
39	78.5	6.3	251	1 HXB4_HUMAN	P17483 homo sapien
40	78.5	6.3	382	1 AVRB_RAT	P38445 rattus norv
41	78.5	6.3	387	1 SGCA_RABIT	Q28686 oryctolagus
42	78.5	6.3	401	1 PD61_RAT	Q94242 rattus norv
43	78.5	6.3	913	1 DDRI1_HUMAN	Q68345 h epithelia
44	78.5	6.3	1180	1 ATY1_HUMAN	Q94111 homo sapien
45	78	6.3	205	1 CYSR_STYR3	Q53854 synecocyst

ALIGNMENTS

RESULT 1
FLJ3L_HUMAN
ID FLJ3L_HUMAN STANDARD: PRT; 235 AA.
AC P45771;
DT 01-OCT-1996 (Ref. 34, Created)
DT 01-OCT-1996 (Ref. 34, Last sequence update)
DT 25-FEB-2003 (Ref. 41, Last annotation update)
DE SL cytokine precursor (fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3L).
DE FLT3LG.
CN Homo sapiens (human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=94195428; PubMed=8145851;
RX Hannon G., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazan J.F., Kastelein R., Hudak S., Wagner J., Matsson J., Lun J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kelnar G., Namikawa R., Rennick D., Boncarollo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
RT *Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of hematopoietic stem cells and is encoded by variant RNAs.*;
RL Nature 368:643-648(1994).
RN [2]
RP MEDLINE=94235842; PubMed=8160375;
RX Zymann S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Spielt R.R., Beckmann M.P., McKenna H.J.;
RT *Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells.*;
RL Blood 83:2795-2801(1994).
RN [3]
RP MEDLINE=94235842; PubMed=8160375;
RX Zymann S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Spielt R.R., Beckmann M.P., McKenna H.J.;
RT *Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells.*;
RL Blood 83:2795-2801(1994).
RN [4]
RP MEDLINE=96032581; PubMed=7566977;
RX Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.S.;
RT *Structural analysis of human and murine flt3 ligand genomic loci.*;
RL Oncogene 11:1165-1172(1995).
RN [5]
RP MEDLINE=20343011; PubMed=10881197;
RX Savvides S.N., Boone T., Kaipus P.A.;
RT *Flt3 ligand structure and unexpected commonalities of helical bundles and cystine knots.*;
RL Nat. Struct. Biol. 7:486-491(2000).
CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
CC -!- SUBUNIT: Homodimer (isoform 2).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms-2:
CC Name-1: Synonyms-Membrane-bound:

CC Isoid-P49771-1: Sequence-Displayed:
 CC Name-2: Synonyms-Soluble;
 CC Isoid-P49771-2: Sequence-VSP_004251, VSP_004252;
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: 004806; AAA17999.1;
 DR EMBL: 003858; AAA19825.1;
 DR EMBL: 029874; AAA90949.1;
 DR EMBL: 029874; AAA90950.1;
 DR PIR: 138440; I38440.
 DR PIR: 139076; I39076.
 DR PDB: 1ETE; 09-JUN-00.
 DR GeneW: HGNC:3766; FLT3LG.
 DR MIM: 600007; -
 DR GO: 0005625; C:soluble fraction: TAS.
 DR GO: 0008284; P:positive regulation of cell proliferation: TAS.
 DR GO: 0007165; P:signal transduction: TAS.
 DR InterPro: IP004213; FLT3_1lg.
 DR Pfam: PF02947; flt3_1lg.1.
 DR Cytokine: Glycoprotein; Transmembrane; Alternative splicing: Signal;
 KW 3D-structure.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 235 SL CYTOKINE.
 FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 POTENTIAL.
 FT DOMAIN 206 235 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 30 111
 FT DISULFID 70 153
 FT DISULFID 119 158
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPLIC 161 178 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 161 178 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 161 178 DSSITPPWMSRRPLKATA -> VETVFRVSDQGLDLITS
 FT VARSPLIC 161 178 (in isoform 2).
 FT VARSPLIC 161 178 /FTid-VSP_004251.
 FT VARSPLIC 161 178 Missing (in isoform 2).
 FT VARSPLIC 161 178 /FTid-VSP_004252.
 FT VARSPLIC 161 178 G -> A (IN REF. 1).
 FT CONFLICT 72 72
 FT STRAND 31 31
 FT TURN 39 40
 FT HELIX 41 49
 FT TURN 50 51
 FT STRAND 53 53
 FT TURN 54 55
 FT STRAND 57 61
 FT STRAND 64 64
 FT TURN 68 70
 FT HELIX 71 87
 FT TURN 88 89
 FT STRAND 90 90
 FT HELIX 92 104
 FT HELIX 106 110
 FT TURN 118 119
 FT STRAND 122 126
 FT HELIX 127 141
 FT TURN 142 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 158 158
 FT SEQUENCE 235 AA; 26416 MW; 73995BF693B4CECF CRC64;

Query Match 100.0%; Score 1242; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.5e-96;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 MTVALPAMSPPTTLLLLSSGLSGTDCSFQHSPISSDAVKITRELSDYLQDPVTV 60
 |||

DB 1 MTVALPAMSPPTTLLLLSSGLSGTDCSFQHSPISSDAVKITRELSDYLQDPVTV 60
 QY 61 ASNZDEDELGGIMRLVLAORMMERIKTVAGSKMGLIERVNTIEHFVTKCAFOPPPSCL 120
 DB 61 ASNZDEDELGGIMRLVLAORMMERIKTVAGSKMGLIERVNTIEHFVTKCAFOPPPSCL 120
 QY 121 RPYOTNISRLQETSEGLVALKRWTRKNSKCLELQOCDDSTLPPWSPRE:EXTAPT 180
 DB 121 RPYOTNISRLQETSEGLVALKRWTRKNSKCLELQOCDDSTLPPWSPRE:EXTAPT 180
 QY 181 APOPLLILLVGCILLAAACIHWCKRRRTPRPGGEVPPVPPSPDILLVEH 235
 DB 181 APOPLLILLVGCILLAAACIHWCKRRRTPRPGGEVPPVPPSPDILLVEH 235

RESULT 2
 FC3L_MOUSE
 ID FC3L_MOUSE STANDARD: PRT: 232 AA.
 AC P49772; Q64085;
 DT 01-OCT-1995 (Rel. 34, Created)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE SL CYTOKINE precursor (Fms-related tyrosine kinase 3 ligand) (FLT3
 DE ligand) (FLT3L).
 CN FLT3LG OR FLT3L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195428; PubMed=8145851;
 RA Hannun C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
 RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Matson J., Luh J.,
 RA Duda G., Martina N., Peterson D., Menon S., Shanefelt A.,
 RA Muench M., Kellner G., Namikawa R., Renick D., Roncarolo M.G.,
 RA Zlotnik A., Hosnet C., Dubreuil P., Birnbaum D., Lee P.;
 RT Ligand for FLT3/FLT3L receptor tyrosine kinase regulates growth of
 RT haematopoietic stem cells and is encoded by variant RNAs.";
 RL Nature 368:643-648(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SIL/J;
 RX MEDLINE=64084791; PubMed=7505204;
 RA Lyman S.D., James L., Vandenbos T., Devries P., Braeel K.,
 RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
 RA Spielt R.R., Fletcher P.A., Maraskovsky E., Fairah T.,
 RA Foxworth D., Williams D.E., Beckmann M.P.;
 RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
 RT receptor: a proliferative factor for primitive hematopoietic cells.";
 RL Cell 75:1157-1167(1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=96032581; PubMed=7566977;
 RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.;
 RT "Structural analysis of human and murine flt3 ligand genomic loci.";
 RL Oncogene 11:1165-1172(1995).
 RN [4]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=95124710; PubMed=7824267;
 RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,
 RA Braeel K., Stocking K., Beckmann M.P., Copeland N.G.,
 RA Cleveland L.S.;
 RT "Identification of soluble and membrane-bound isoforms of the murine
 RT flt3 ligand generated by alternative splicing of mRNAs.";
 RL Oncogene 10:149-157(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA McClanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Frenzel-Bacon K., Matson J., Tsai S., Luh J., Gularnes M.J.,
 RA Matzel M.-G., Kosnet O., Birnbaum D., Hannun C.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBA databases.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:45:12 : Search time 62.5122 Seconds
(without alignments)
969.778 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MYVLAPAMSPPTTYLLILLLL.....RPGEOVPPVPSPODLLLVEH 235

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_protent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895.5	72.1	294	Q9M2V0	Q9M2V0 canis famili
2	894.5	72.0	291	Q9M2U9	Q9M2U9 felis silve
3	840	67.6	292	Q9GKE0	Q9GKE0 bos taurus
4	835	67.2	292	Q9MNM1	Q9MNM1 bos taurus
5	746	60.1	274	Q9GKD9	Q9GKD9 bos taurus
6	602.5	48.5	172	Q61104	Q61104 mus muscula
7	578	46.5	169	Q9VCH4	Q9VCH4 mus muscula
8	112.5	9.1	579	Q9LGC8	Q9LGC8 oryza sativ
9	110	8.9	219	Q8DKT7	Q8DKT7 synechococc
10	105	8.5	208	Q8L418	Q8L418 oryza sativ
11	100.5	8.1	1809	Q8V1M6	Q8V1M6 mus musculi
12	97.5	7.9	669	Q8GYA4	Q8GYA4 arabidopsis
13	95.5	7.7	439	Q8N775	Q8N775 homo sapien
14	95.5	7.7	658	Q8H785	Q8H785 arabidopsis
15	95.5	7.7	1240	Q9DMH8	Q9DMH8 rat cytochr
16	93.5	7.5	658	Q9C5T0	Q9C5T0 arabidopsis

17	93	7.5	1217	5	Q17989	Q17989 caenorhabdi
18	92.5	7.4	387	11	Q8VD70	Q8VD70 mus musculu
19	92.5	7.4	1400	5	Q9VDD2	Q9VDD2 drosophila
20	92	7.4	251	4	Q9KAD2	Q9KAD2 homo sapien
21	91.5	7.4	287	16	Q8DH33	Q8DH33 synechococ
22	91.5	7.4	308	11	Q8BP15	Q8BP15 mus musculu
23	91.5	7.4	674	11	Q8K4C2	Q8K4C2 mus musculu
24	89.5	7.2	474	5	Q17610	Q17610 caenorhabdi
25	88.5	7.1	238	16	Q8YWX3	Q8YWX3 anabaena sp
26	88.5	7.1	270	4	Q9DMT1	Q9DMT1 homo sapien
27	88.5	7.1	356	2	Q8KR32	Q8KR32 yeastina ps
28	88.5	7.1	404	10	Q9AWJ4	Q9AWJ4 oryza sativ
29	88.5	7.1	579	4	Q8N158	Q8N158 homo sapien
30	88.5	7.1	1267	10	Q943D5	Q943D5 oryza sativ
31	88.5	7.1	1386	4	Q75064	Q75064 homo sapien
32	88	7.1	250	6	Q9GKE2	Q9GKE2 sus scrofa
33	88	7.1	753	12	Q56971	Q56971 kenneya ye
34	88	7.1	791	11	Q8K4Z5	Q8K4Z5 mus musculu
35	88	7.1	791	11	Q8C175	Q8C175 mus musculu
36	88	7.1	791	11	Q8C128	Q8C128 mus musculu
37	88	7.1	791	11	Q8C0M7	Q8C0M7 mus musculu
38	87.5	7.0	470	10	Q9LUI1	Q9LUI1 arabidopsis
39	87.5	7.0	564	10	Q8L729	Q8L729 spinacia ol
40	87.5	7.0	946	10	Q22015	Q22015 cylindrothe
41	87	7.0	510	5	Q44018	Q44018 leishmania
42	87	7.0	5317	5	Q8TA74	Q8TA74 hemientrot
43	85.5	7.0	299	6	Q9T7T9	Q9T7T9 bos taurus
44	85.5	7.0	598	4	Q8NHJ7	Q8NHJ7 homo sapien
45	86	6.9	255	11	Q9D3J3	Q9D3J3 mus musculu

ALIGNMENTS

RESULT 1

ID	Q9M2V0	PRELIM-NARY:	PRT:	294 AA.
AC	Q9M2V0:			
DT	01-OCT-2000 (TREMBL)	15, Created		
DT	01-OCT-2000 (TREMBL)	15, last sequence update		
DT	01-MAR-2003 (TREMBL)	23, last annotation update		
DE	Hit3 ligand.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID:9615.			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20358731; PubMed-10902925;			
RA	Yang S., Sim G.K.;			
RT	"Molecular cloning of canine and feline hit3 ligand reveals high			
RT	degree of similarity to the human and mouse homologue but uniquely			
RT	long cytoplasmic domain."			
RI	DNA Seq. 11-163-166(2000).			
DR	EMBL: AF155148; AAF87088.1; -			
DR	HSPB: P49771; HTE.			
DR	InterPro: IP004213; F1C3_119.			
DR	Pfam: PF02947; F1C3_119; 1.			
SC	SEQUENCE 294 AA: 32394 MW: 68599176.3874A3CD CRC64:			

Query Match	72.1%	Score 895.5;	DB 6;	Length 294;
Best Local Similarity	77.1%	Pred. NO. 9.7e-79;		
Matches 182;	Conservative 12;	Mismatches 35;	Indels 7;	Gaps 3;
QY	1	MYVLAPAMSPPTTYLLILLSSGSGTQDSFGHSPISDFAVKRELSDYLLQDYHVTY	60	
DB	1	MYVLAPAMSPPTTYLLILLSSGSGTQDSFGHSPISDFAVKRELSDYLLQDYHVTY	60	
QY	61	ASNLDELGGLMRVLAQRMERUKTVAGSKWGLLEEVNTHIEVTGCAFPPEPSC	120	
DB	61	ASNLDELGGLMRVLAQRMERUKTVAGSKWGLLEEVNTHIEVTGCAFPPEPSC	120	
QY	121	RFVGTNISRLLQETSEQLVAKKPIITRONFSRLIELOQCPDSSTLPPWSPRLERAP	180	
DB	121	RFVGTNISRLLQETSEQLVAKKPIITRONFSRLIELOQCPDSSTLPPWSPRLERAP	180	

DB 121 REVQTNISHLQDTSQQLAALKPWTRNFSQCLEQCPDSSSTLPVPRSPALATAP 180
 QY 181 APOPP-LLLLLLLPVGLLLAAACLMH-CRTTRRTTRPRGCVPPVPS-----PGD 229
 DB 181 APOAPRLLLLLLLPVALLMLSTAMCLHMRRRRRRSPYPGEQRTLPFSERSHLPED 236

RESULT 2

Q9MZU9 PRELIMINARY: PRT: 291 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Flt3 ligand.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20356731; PubMed=10902925;
 RA Yang S., Sim G.K.:
 RT Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain.*
 RL DNA Seq. 11:163-166(2000).
 DR EMBL: AF155149; AAF87089.1; -
 DR HSSP: P49771; IETE.
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; Flt3_119; 1.
 SQ SEQUENCE 291 AA: 32459 MW: 8F85A10A5EA0DC5 CRC64:

Query Match 72.0%; Score 894.5; DB 6; Length 291;
 Best Local Similarity 80.5%; Pred. No. 1,2e-78;
 Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MVLAPAWSPPTT-LLLLLLLSGLSGTQDCSFQSPHSPISDFAVKIRELSLYLLQDPVTV 60
 DB 1 MVLAPAWSPPTT-LLLLLLLSGLSGTQDCSFQSPHSPISDFAVKIRELSLYLLQDPVTV 60
 QY 61 ASVLQDEELCGGLWRLVLAQRMMERLKTVAAGSMOGLLEVRNTEIHFTVKCAFQPPSPCL 120
 DB 61 ASVLQDEELCGGLWRLVLAQRMMERLKTVAAGSMOGLLEVRNTEIHFTVKCAFQPPSPCL 120
 QY 121 REVQTNISRLQETSEQLVALKPWTRQNSRCLQLQCPDSSSTLPVPRSPALATAP 180
 DB 121 REVQTNISRLQETSEQLVALKPWTRQNSRCLQLQCPDSSSTLPVPRSPALATAP 180
 QY 181 APOPP-LLLLLLLPVGLLLAAACLMH-CRTTRRTTRPRGCVPPVPS-----PGD 229
 DB 181 APOAPRLLLLLLLPVALLMLSTAMCLHMRRRRRRSPYPGEQRTLPFSERSHLPED 221

RESULT 3

Q9GKE0 PRELIMINARY: PRT: 292 AA.

DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Flt3 ligand isoform-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN
 RP SOURCE FROM N.A.
 RX MEDLINE=20570936; PubMed=11120823;
 RA Wang W., Brown W.C., Palmer G.H.:
 RT Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain

RT required for receptor binding and function using naturally occurring
 RT ligand isoforms.*
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL: AF282985; AAF99322.1; -
 DR HSSP: P49771; IETE.
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; Flt3_119; 1.
 SQ SEQUENCE 292 AA: 32390 MW: D68B9FD79221202D CRC64:

Query Match 67.6%; Score 840; DB 6; Length 292;
 Best Local Similarity 76.3%; Pred. No. 2,3e-73;
 Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MVLAPAWSPPTT-LLLLLLLSGLSGTQDCSFQSPHSPISDFAVKIRELSLYLLQDPVTV 59
 DB 1 MVLAPAWSPPTT-LLLLLLLSGLSGTQDCSFQSPHSPISDFAVKIRELSLYLLQDPVTV 60
 QY 60 VASNLQDEELCGGLWRLVLAQRMMERLKTVAAGSMOGLLEVRNTEIHFTVKCAFQPPSPCL 119
 DB 61 VASNLQDEELCGGLWRLVLAQRMMERLKTVAAGSMOGLLEVRNTEIHFTVKCAFQPPSPCL 120
 QY 120 REVQTNISRLQETSEQLVALKPWTRQNSRCLQLQCPDSSSTLPVPRSPALATAP 179
 DB 121 REVQTNISRLQETSEQLVALKPWTRQNSRCLQLQCPDSSSTLPVPRSPALATAP 180
 QY 180 TAPOPP-LLLLLLLPVGLLLAAACLMH-CRTTRRTTRPRGCVPPVPS-----PGD 229
 DB 181 PGOSPLLLLLLLPVALLMLSTAMCLHMRRRRRRSPYPGEQRTLPFSERSHLPED 224

RESULT 4

Q8NMW1 PRELIMINARY: PRT: 292 AA.

DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, last annotation update)
 DE Flt3 ligand.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN
 RP SEQUENCE FROM N.A.
 RA Hirono H., Momotani E.:
 RT Cloning of a cDNA for bovine flt3 ligand.*
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB051841; BAB79634.1; -
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; Flt3_119; 1.
 SQ SEQUENCE 292 AA: 32388 MW: 2A797E0C1199C1D9 CRC64:

Query Match 67.2%; Score 835; DB 6; Length 292;
 Best Local Similarity 75.9%; Pred. No. 7,1e-73;
 Matches 170; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

QY 1 MVLAPAWSPPTT-LLLLLLLSGLSGTQDCSFQSPHSPISDFAVKIRELSLYLLQDPVTV 59
 DB 1 MVLAPAWSPPTT-LLLLLLLSGLSGTQDCSFQSPHSPISDFAVKIRELSLYLLQDPVTV 60
 QY 60 VASNLQDEELCGGLWRLVLAQRMMERLKTVAAGSMOGLLEVRNTEIHFTVKCAFQPPSPCL 119
 DB 61 VASNLQDEELCGGLWRLVLAQRMMERLKTVAAGSMOGLLEVRNTEIHFTVKCAFQPPSPCL 120
 QY 120 REVQTNISRLQETSEQLVALKPWTRQNSRCLQLQCPDSSSTLPVPRSPALATAP 179
 DB 121 REVQTNISRLQETSEQLVALKPWTRQNSRCLQLQCPDSSSTLPVPRSPALATAP 180
 QY 180 TAPOPP-LLLLLLLPVGLLLAAACLMH-CRTTRRTTRPRGCVPPVPS-----PGD 229
 DB 181 PGOSPLLLLLLLPVALLMLSTAMCLHMRRRRRRSPYPGEQRTLPFSERSHLPED 224

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:43:17 : Search time 59.485 Seconds
(Without alignments)
616.388 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MVLAPAWSPNSSLLILL.....MORARRRGELHGVPLPSP 231

Scoring table: BIOSUM62
Gapop 10.0 , Capext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1223	100.0	23	16 AAR67540 Mouse flt-3 ligand
2	1223	100.0	231	20 AAM67768 Murine flt-3 ligand
3	1223	100.0	231	22 AAB20186 Mouse flt-3 ligand
4	1223	100.0	231	24 AAG74238 Mouse flt-3 ligand
5	1212.5	99.1	232	15 AAR67177 Mouse MGL10/T118
6	1208.5	98.6	232	22 AAB20189 Mouse flt-3 ligand
7	1006	82.3	288	22 AAU02129 flt-3 ligand (Fv)
8	1004	82.1	189	22 AAB20187 Mouse flt-3 ligand
9	1004	82.1	189	23 AAB82182 Murine flt-3 ligand

10	1004	82.1	189	23 AAB81114	flt-3 ligand (Fv) e
11	1004	82.1	289	23 AAB82383	Murine flt-3 ligand
12	1004	82.1	289	23 AAB81115	Flt-E7 fusion prote
13	1004	82.1	528	23 AAB81116	Flt-E7-GFP fusion p
14	879	71.9	172	22 AAB20191	Mouse flt-3 ligand
15	879	71.9	220	22 AAB20188	Mouse flt-3 ligand
16	879	71.9	220	22 AAB20190	Mouse flt-3 ligand
17	774	63.3	294	21 AAY58204	Canine flt-3 ligand
18	772.5	63.2	235	16 AAR66175	Human S86/S109 flt
19	772.5	63.2	235	22 AAB20194	Human flt-3 ligand
20	768.5	62.8	235	16 AAR67541	Human flt-3 ligand
21	768.5	62.8	235	20 AAM67769	Human flt-3 ligand
22	768.5	62.8	235	21 AAY69719	Full length wild t
23	768.5	62.8	235	22 AAB20192	Human flt-3 ligand
24	768.5	62.8	235	23 AA019091	C neofornas anti g
25	768.5	62.8	235	23 AHC31626	Human Flt-3L protei
26	768.5	62.8	235	23 AHB08129	Human Flt-3L poly
27	768.5	62.8	235	24 AAG79949	Secreted human pro
28	768.5	62.8	235	24 AAG74239	Human flt-3 ligand
29	763.5	62.4	235	24 AAG79950	Secreted human pro
30	761	62.2	291	21 AAY58210	Feline flt-3 ligan
31	692	56.6	212	21 AAY69721	Human flt-3 mutain
32	687	56.2	209	21 AAY69724	Human flt-3 mutain
33	686	56.1	209	19 AAM69007	Human flt-3 mutain
34	686	56.1	209	19 AAY69720	Human flt-3 mutain
35	686	56.1	209	21 AAY69725	Mature wild type h
36	685	56.0	209	21 AAY69725	Human flt-3 mutain
37	682	55.8	209	21 AAY69725	Human flt-3 mutain
38	682	55.8	209	21 AAY69725	Human flt-3 mutain
39	682	55.8	209	21 AAY69729	Human flt-3 mutain
40	680	55.6	209	21 AAY69722	Human flt-3 mutain
41	679.5	55.6	208	21 AAY58206	Human flt-3 mutain
42	679	55.5	209	21 AAY69728	Canine mature flt-
43	668	54.6	276	21 AAY58207	Human flt-3 mutain
44	666.5	54.5	265	21 AAY58211	Canine flt-3 ligan
45	663.5	54.3	185	22 AAB20195	Feline mature flt-
					Human flt-3 ligand

ALIGNMENTS

RESULT 1	
ID AAR67540	standard; Protein: 231 AA.
XX AAR67540:	
AC	25-MAR-2003 (updated)
XX	05-MAR-1995 (first entry)
UT	Mouse flt-3 ligand.
XX	
CE	Mouse flt-3 ligand.
XX	
KW	Flt-3 ligand; flt-3; anemia; cancer; AIDS; gene therapy.
XX	
OS	Mus sp.
XX	
FH	Key
FT	peptide
FT	Location/Qualifiers
FT	1..27
FT	/label= Sig_peptide
FT	28..188
FT	/label= Extracellular_domain
FT	189..211
FT	/label= Transmembrane_domain
FT	212..231
FT	/label= Cytoplasmic_domain
FT	
FT	Domain
FT	
PN	FP627487-A2.
XX	
PD	07-DEC-1994.
XX	
PF	19-MAY-1994: 94EP-0303575.
XX	
PR	24-MAY-1993: 93US-0068394.

```

PR 12-AUG-1993: 93US-0106463.
PR 25-AUG-1993: 93US-0111758.
PR 03-DEC-1993: 93US-0162407.
PR 07-MAR-1994: 94US-0209502.
PR 11-MAY-1994: 94US-0243545.
XX
XX (IMMUNEX CORP.
PA Beckmann MP, Lyman SD:
PI WPI: 1995-008971/02.
XX N-PSDB: AAO79076.
DR
XX
XX Isolated ligands for flt 3 receptors - useful for treating
PT anaemia, AIDS and various cancers
PI
XX
XX Disclosure: Page 25-27: 33pp: English.
PS
XX
XX cDNA encoding mouse flt3 ligand (flt3-L) was isolated from a
CC cDNA library of T-cell line P7B-0.3M in CV-1/EBNA-1 cells
CC using a slide autoradiography method. flt3-L stimulates
CC production of progenitor and stem cells, and can be used e.g.
CC in gene therapy protocols.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
XX Sequence 231 AA:
SQ
Query Match 100.0%: Score 1223: DB 16: Length 231:
Best Local Similarity 100.0%: Pred. No. 5.5e-115:
Matches 231: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKRELTHLKDYPVT 60
DB 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKRELTHLKDYPVT 60
QY 61 VAVNLQDEKCKALMSFLAORMIEOLKTVAGSKMOTLEDVNTETHFVTSCTFOPLPEC 120
DB 61 VAVNLQDEKCKALMSFLAORMIEOLKTVAGSKMOTLEDVNTETHFVTSCTFOPLPEC 120
QY 121 LRFVQINISHLKDTCTQLALKPCIGKACQNSRCLEVOQCPDSSSTLLPPRSPALEAT 180
DB 121 LRFVQINISHLKDTCTQLALKPCIGKACQNSRCLEVOQCPDSSSTLLPPRSPALEAT 180
QY 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231
DB 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231

RESULT 2
AAB67768
ID AAB67768 standard: Protein: 231 AA.
XX
XX AAB67768:
AC
XX
XX 25-MAR-1999 (first entry)
DE Murine flt3-ligand.
XX
XX Antigen-specific peripheral immune tolerance: flt3-ligand: flt3-L;
KW immunogenic; autoimmune disease: organ transplantation: food allergy;
XX tissue transplantation.
XX
XX Mus sp.
OS
XX
XX MO9857655-A1.
XX
XX 23-DEC-1998.
XX
XX 12-JUN-1998: 98MO-US12085.
XX
XX 17-JUN-1997: 97US-0877421.
XX
XX (IMMUNEX CORP.

```

```

XX
XX Abbott NM, Kowat AM, Viney JL:
PT
XX
XX WPI: 1999-070422/06.
DR
XX N-PSDB: AAB81505.
XX
XX Methods for initiating or enhancing antigen specific immune
PT tolerance - by using murine or human flt3 ligand
PI
XX
XX Claim 1: Page 12: 25pp: English.
PS
XX
XX A method has been developed of initiating or enhancing: (i) an antigen-
CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
CC immunogenic molecule by addition of a polypeptide, before, after or with
CC the mucosal administration of an immunotolerising amount of the antigen
CC or therapeutic molecule, respectively. The polypeptide is capable of
CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
CC acids 28-y of human flt3-L, where y is an amino acid between 163-235;
CC and c) a polypeptide that has at least 90% identity to the polypeptides
CC of either (a) or (b). The method ameliorates the effects of autoimmune
CC diseases, food allergies or organ or tissue rejection following
CC transplantation. Administration of flt3-L allows lower doses of antigens
CC to be used in vivo for mucosally administered antigens. The present
CC sequence represents murine flt3-L.
CC
XX
XX Sequence 231 AA:
SQ
Query Match 100.0%: Score 1223: DB 20: Length 231:
Best Local Similarity 100.0%: Pred. No. 5.5e-115:
Matches 231: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKRELTHLKDYPVT 60
DB 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKYKFKRELTHLKDYPVT 60
QY 61 VAVNLQDEKCKALMSFLAORMIEOLKTVAGSKMOTLEDVNTETHFVTSCTFOPLPEC 120
DB 61 VAVNLQDEKCKALMSFLAORMIEOLKTVAGSKMOTLEDVNTETHFVTSCTFOPLPEC 120
QY 121 LRFVQINISHLKDTCTQLALKPCIGKACQNSRCLEVOQCPDSSSTLLPPRSPALEAT 180
DB 121 LRFVQINISHLKDTCTQLALKPCIGKACQNSRCLEVOQCPDSSSTLLPPRSPALEAT 180
QY 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231
DB 181 ELPEPRRQRLLLLLLPLTLVLLAAAGLKWQARRRGELHGVPLPSHP 231

RESULT 3
AAB20186
ID AAB20186 standard: Protein: 231 AA.
XX
XX AAB20186:
AC
XX
XX 14-MAY-2001 (first entry)
DE Mouse Flt-3 ligand.
XX
XX Flt-3 ligand: Fms-like tyrosine kinase: mouse; vaccine:
KW immunotherapy: therapy: tumour; cancer; melanoma; glioma;
XX lymphoma; autoimmune disease: infection; gene therapy.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
XX 1..27
XX Peptide /label= Signal_peptide
XX 28..231
XX Protein /label= Mature_protein
XX 28..188
XX Domain /label= Extracellular_domain
XX 189..211

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:52:22 : Search time 20.324 Seconds

(Without alignments)
480.899 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MTVALPAPMSPNSLLILL...MQRARRGELHPGVLPSP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCrus_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1223	100.0	231	1	US-08-243-545-2
2	1223	100.0	231	2	US-08-993-962-2
3	1223	100.0	231	3	US-09-160-841-2
4	1223	100.0	231	5	PCT-US94-05365-2
5	1220	99.8	231	1	US-08-220-3798-7
6	1220	99.8	231	5	PCT-US94-03866-6
7	774	63.3	294	4	US-09-322-409-7
8	774	63.3	294	4	US-09-451-527-7
9	768.5	62.8	235	1	US-08-243-545-6
10	768.5	62.8	235	2	US-08-993-962-6
11	768.5	62.8	235	3	US-09-160-841-6
12	768.5	62.8	235	3	US-09-109-100-1
13	768.5	62.8	235	5	PCT-US94-05365-6
14	761	62.2	291	4	US-09-322-409-44
15	761	62.2	291	4	US-09-451-527-44
16	724.5	59.2	137	3	US-09-109-100-19
17	692	56.6	212	3	US-09-109-100-10
18	687	56.2	209	3	US-09-109-100-15
19	686	56.1	209	3	US-09-109-100-14
20	686	56.0	209	3	US-09-109-100-18
21	685	55.8	209	3	US-09-109-100-16
22	682	55.8	209	3	US-09-109-100-9
23	682	55.8	209	3	US-09-109-100-12
24	682	55.8	209	3	US-09-109-100-17
25	680	55.6	209	3	US-09-109-100-11
26	679.5	55.6	268	4	US-09-322-409-23
27	679.5	55.6	268	4	US-09-451-527-23

28	679	55.5	209	3	US-09-109-100-13	Sequence 13, Appl
29	678	55.4	209	3	US-09-109-100-8	Sequence 8, Appl
30	668	54.6	276	4	US-09-322-409-26	Sequence 26, Appl
31	668	54.6	276	4	US-09-451-527-26	Sequence 26, Appl
32	666.5	54.5	265	4	US-09-322-409-49	Sequence 49, Appl
33	666.5	54.5	265	4	US-09-451-527-49	Sequence 49, Appl
34	573.5	46.9	250	4	US-09-322-409-11	Sequence 31, Appl
35	573.5	46.9	250	4	US-09-451-527-11	Sequence 31, Appl
36	216	17.7	42	5	PCT-US94-05150-17	Sequence 17, Appl
37	135	11.0	28	5	PCT-US94-05150-12	Sequence 12, Appl
38	105	8.6	22	5	PCT-US94-05150-10	Sequence 10, Appl
39	95.5	7.8	909	2	US-08-310-912A-142	Sequence 142, App
40	95.5	7.8	909	3	US-09-301-085-142	Sequence 142, App
41	95.5	7.8	909	5	PCT-US95-04589-142	Sequence 142, App
42	92	7.5	885	2	US-08-310-912A-2	Sequence 2, Appl
43	92	7.5	885	3	US-08-841-089-2	Sequence 2, Appl
44	92	7.5	885	3	US-09-101-085-2	Sequence 2, Appl
45	92	7.5	885	5	PCT-US95-04570-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-243-545-2
Sequence 2, Application US/08243545
Patent No. 554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for Flt3/Tlk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 5, University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version 4.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELEPHONE: (206) 587-0436
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-2

Query Match 100.0%; Score 1223; DB 1; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.7e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFELTHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFELTHLKDYPT 60
QY 61 VAVNLODEKHCALMSLELAQRMIEQLTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
DB 61 VAVNLODEKHCALMSLELAQRMIEQLTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSFALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSFALAEAT 180
QY 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231
DB 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231

RESULT 2
US-08-993-962-2
Sequence 2, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-378-2

Query Match 100.0%; Score 1223; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.7e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFELTHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYSHSPSSNFKVRFELTHLKDYPT 60
QY 61 VAVNLODEKHCALMSLELAQRMIEQLTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
DB 61 VAVNLODEKHCALMSLELAQRMIEQLTVAGSKMOTLLEDVNTLHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSFALAEAT 180
DB 121 LRFVQTNISHLKDTCTQLLALPKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSFALAEAT 180
QY 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231
DB 181 ELPEPRRQQLLLILLPLTLVLLAAAGLRWQARRRGELHPGVPLPSHP 231

RESULT 3
US-09-60-841-2
Sequence 2, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 15, 2003, 15:57:23 : Search time 39.6567 Seconds
(without alignments)
849,940 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MVTIAPAMSPNSILLLL.....MQRARRGELHRCVLPSPSP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Published Applications, AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCW_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCW_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	231	7	US-08-994-468-2
2	1223	100.0	231	9	US-09-448-378-2
3	1223	100.0	231	10	US-09-983-806-2
4	1223	100.0	231	12	US-10-314-035-2
5	1223	100.0	231	14	US-10-095-449-2
6	774	63.3	294	12	US-10-262-439-7
7	774	63.3	294	15	US-10-218-654-7
8	768.5	62.8	235	9	US-08-994-468-6
9	768.5	62.8	235	9	US-09-448-378-1
10	768.5	62.8	235	10	US-09-983-806-6
11	768.5	62.8	235	10	US-09-904-536-1
12	768.5	62.8	235	12	US-10-314-035-6
13	768.5	62.8	235	14	US-10-095-449-6
14	768.5	62.8	235	15	US-10-241-927-2
15	761	62.2	291	12	US-10-262-439-44

16	761	62.2	291	15	US-10-218-654-44	Sequence 44, Appl
17	724.5	59.2	137	10	US-09-904-536-19	Sequence 19, Appl
18	592	56.6	212	10	US-09-904-536-10	Sequence 10, Appl
19	687	56.2	209	10	US-09-904-536-15	Sequence 15, Appl
20	686	56.1	209	10	US-09-904-536-14	Sequence 14, Appl
21	686	56.1	209	10	US-09-904-536-18	Sequence 18, Appl
22	685	56.0	209	10	US-09-904-536-16	Sequence 16, Appl
23	682	55.8	209	10	US-09-904-536-9	Sequence 9, Appl
24	682	55.8	209	10	US-09-904-536-12	Sequence 12, Appl
25	682	55.8	209	10	US-09-904-536-17	Sequence 17, Appl
26	680	55.6	209	10	US-09-904-536-11	Sequence 11, Appl
27	679.5	55.6	268	12	US-10-262-439-23	Sequence 23, Appl
28	679.5	55.6	268	15	US-10-218-654-23	Sequence 23, Appl
29	679	55.5	209	10	US-09-904-536-13	Sequence 13, Appl
30	678	55.4	209	10	US-09-904-536-8	Sequence 8, Appl
31	668	54.6	276	12	US-10-262-439-26	Sequence 26, Appl
32	668	54.5	276	15	US-10-218-654-25	Sequence 25, Appl
33	666.5	54.5	265	12	US-10-262-439-49	Sequence 49, Appl
34	666.5	54.5	265	15	US-10-218-654-49	Sequence 49, Appl
35	573.5	46.9	250	12	US-10-262-439-31	Sequence 31, Appl
36	573.5	46.9	250	15	US-10-218-654-31	Sequence 31, Appl
37	562	46.4	156	15	US-10-053-355A-1	Sequence 1, Appl
38	95.5	7.8	909	10	US-09-867-852-142	Sequence 142, App
39	94	7.7	355	10	US-09-948-018-2	Sequence 2, Appl
40	92	7.5	885	10	US-09-867-852-2	Sequence 2, Appl
41	91.5	7.5	941	15	US-10-225-567A-436	Sequence 436, App
42	89.5	7.3	874	9	US-09-826-508-26	Sequence 26, Appl
43	89.5	7.3	941	9	US-09-818-879-47	Sequence 47, Appl
44	89.5	7.3	941	9	US-09-211-755B-47	Sequence 47, Appl
45	89.5	7.3	941	10	US-09-793-139-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-08-994-468-2

Sequence 2, Appl: US-08-994-468

Publication No. US20030148516A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

Researcher: M. Patricia

TITLE OF INVENTION: Ligands for f113/f1k-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version 45.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/994-468

FILING DATE: 19-Dec-1997

CLASSIFICATION: <Unknown>

PRIO: APPLICATION DATA:

APPLICATION NUMBER: 08/162,407

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/058,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 231 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-994-468-2

Query Match 100.0%; Score 1223; DB 7; Length 231;

Best Local Similarity 100.0%; Pred. No. 2, 1e-108;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVRFELTHLLKDYPT 60

DB 1 MTVALAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVRFELTHLLKDYPT 60

OY 61 VAVNLODEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLPDVNTLHFVTSCTFOPLPFC 120

DB 61 VAVNLODEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLPDVNTLHFVTSCTFOPLPFC 120

OY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

OY 181 ELPEPRRQRLLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

DB 181 ELPEPRRQRLLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

RESULT 2

US-09-448-378-2

Sequence 2, Application US/09448378

Patent No. US20020034517A1

GENERAL INFORMATION:

APPLICANT: Bristol, Kenneth

TITLE OF INVENTION: Dendritic Cell Stimulatory Factor

FILE REFERENCE: 2836-D

CURRENT APPLICATION NUMBER: US/09/448.378

CURRENT FILING DATE: 1999-11-23

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 231

TYPE: PRT

ORGANISM: Mus sp.

US-09-448-378-2

Query Match 100.0%; Score 1223; DB 7; Length 231;

Best Local Similarity 100.0%; Pred. No. 2, 1e-108;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVRFELTHLLKDYPT 60

DB 1 MTVALAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVRFELTHLLKDYPT 60

OY 61 VAVNLODEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLPDVNTLHFVTSCTFOPLPFC 120

DB 61 VAVNLODEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLPDVNTLHFVTSCTFOPLPFC 120

OY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

OY 181 ELPEPRRQRLLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

DB 181 ELPEPRRQRLLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

RESULT 3

US-09-983-806-2

Sequence 2, Application US/09983806

Patent No. US20020107365A1

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for F113/L1K-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Stephen L. Malaska, Immunex Corporation

SUBJECT: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version 4.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/983,806

FILING DATE: 25-Oct-2001

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/444,626

FILING DATE: 19-MAY-1995

APPLICATION NUMBER: US 08/162,407

FILING DATE: 03-DEC-1993

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 28-3-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 231 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-983-806-2

Query Match 100.0%; Score 1223; DB 10; Length 231;

Best Local Similarity 100.0%; Pred. No. 2, 1e-108;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVRFELTHLLKDYPT 60

DB 1 MTVALAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVRFELTHLLKDYPT 60

OY 61 VAVNLODEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLPDVNTLHFVTSCTFOPLPFC 120

DB 61 VAVNLODEKCKALMSLFLAQRWIEQLKTVAGSKMOTLLPDVNTLHFVTSCTFOPLPFC 120

OY 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

DB 121 LRFVQTNISHLKDTQTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPTALEAT 180

OY 181 ELPEPRRQRLLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

DB 181 ELPEPRRQRLLLLLLPLTLVLLAAWGLRMQARRRGELHFGVPLPSHP 231

[illegible]

RESULT 2
S43291
ELT3/FLK2 Ligand (clone T118) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43291
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazzone, J.F.; Kottmann, H.; Felt, A.; Muench, M.; Keisner, G.; Nankkawa, R.; Rennick, D.; Roncarolo, M.G.; Clinton, P.
Nucleotide: 643-648, 1994
A>Title: Ligand for ELT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428; PMID:8145851
A:Accession: S43291
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-220 <HAX>

```

Query Match 879; DB 2; Length 220;
Best Local Similarity 82.3%; Pred. No. 1,le-70;
Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY      1 MTVLPAWSPNSLLILLILSPCLRGTPDCYFSHSPISSNPKYKFRLLDHLKDYD;PVT 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       1 MTLVLPASPNSLLILLILSPCLRGTPDCYFSHSPISSNPKYKFRLLDHLKDYD;PVT 60
QY      61 VAVNLDGKHKKALMSLFLAQRWTEQLKTAVGSKMOTLLDEYVNEIHVYTSCTFOPL;EPC 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       61 VAVNLDGKHKKALMSLFLAQRWTEQLKTAVGSKMOTLLDEYVNEIHVYTSCTFOPL;EPC 120
QY      121 LRFVQTNISHLKDKTCTQLLAKPCIGKACONFSDHCEVOCOPDOSTLPLPS;---DIA 176
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       121 LRFVQTNISHLKDKTCTQLLAKPCIGKACONFSDHCEVOCOPDONG---GPRACIHNGAT; 177
QY      177 LEATLEPPRRQILL-----LLPLPLTVYLLAA 206
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       178 LTRALRLTVCCPLCLPLVGTSHMPLPYFLFLSS 212

```

```

RESULT 3
158343
f1t3_ligand isoform 5H - mouse
C.Species: Mus sp. (mouse)
C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1996
C.Accession: I58343
R.Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, D.
Oncogene 10: 149-157, 1995
A.Title: Identification of soluble and membrane-bound isoforms of the murine f1t3 ligand
A.Reference number: I58343; MUID:95124710; PMID:7824267
A.Status: Preliminary; translated from GB/EMBL/CDBJ
A.Molecule type: mRNA
A.Residues: 1-220 <RES>
A.Cross-references: GB:S76459; NID:q913479; PIDN:AAB33069.1; PID:q913480

Query Match      71.9%; Score 879; DB 2; Length 220;
Best Local Similarity 82.3%; Pred. No. 11e-70;
Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY      1 MTLVAPASPNSSULLLLLLLSPCLRGTPDCYFSHPRISSNKKVVFRELTHTLMDRYVT 60
|||||

```

```

Lb 1 ATVALPAMSPNSS:LLLLLLLLLPCRTPPGCVESHSPSSSNFKVKKFRELIDHLKICVPYT 60
Cy 63 VAVVLQDEKHKAKAMSLFLAQRWIEOLKTVAGSKMOTLEDVNIETIFVTSICFQPLPEC 120
Db 61 VAVNIQDEKHKAKAMSLFLAQRWIEOLKTVAGSKMOTLEDVNIETIFVTSICFQPLPEC 120
Cy 121 LRFQNTSHLKCITCTOLLAKPCIGSKAONSRCLVEVOCOPDSSHTLPPAS:---PIA 176
Db 121 LRFQNTSHLKCITCTOLLAKPCIGSKAONSRCLVEVOCOPDSSHTLPPAS:---PIA 176
Cy 121 LRFQNTSHLKCITCTOLLAKPCIGSKAONSRCLVEVOCOPDSSHTLPPAS:---PIA 176
Db 121 LRFQNTSHLKCITCTOLLAKPCIGSKAONSRCLVEVOCOPDSSHTLPPAS:---PIA 176
Cy 177 LEATFELEPRRCGLL:-----LLLLPLETLEVLAA 206
Db 177 LEATFELEPRRCGLL:-----LLLLPLETLEVLAA 206
Cy 178 LTAALLTVCQGLLLPLVQTSNMFELPYFLISLSS 212
Db 178 LTAALLTVCQGLLLPLVQTSNMFELPYFLISLSS 212

```

```

RESULT 4
138440
1-23 ligand - human
C.Species: Homo sapiens (Man)
C.Date: 29-May-1998 #sequence-Revision 29-May-1998 #text-Change 01-Dec-2000
C.Accession: 138440; I390755; S43292
R.Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Eschobar, S.S.; Dornier
Slood 83, 2795-2801, 1994
A.Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor for
A.Reference number: 138440; MIMD:94235842; PMID:8180375
A.Accession: 138440
A.Status: preliminary; translated from GE/EMBL/DBD
A.Molecule type: mRNA
A.Res.dues: 1-235 <RNA>

```

A:Cross-references: EMBL:U00858; NID:494978; PID:494979
R:Lyman, S.D.; Stocking, K.; Davison, R.; Fletcher, A.; Johnson, I.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine fil3 ligand genomic loci.
A:Reference number: 139075; MUID:36032581; PMID:7566977
A:Accession: 139075
A>Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RE>
A:Cross-references: EMBL:U29874; NID:1072036; PID:AA09049, 1; PID:q1072037
R:Hamam, C.; Culpepper, J.; Campbell, D.; McCleanahan, I.; Zurawski, S.; Bazan, J.F.;
felt, A.; Mench, M.; Kellner, G.; Nankkava, R.; Rennick, D.; Koncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A:Title: L3 and for fil3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43292; MUID:94195428; PMID:8145851
A:Accession: S43292
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', '73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PID:AA1799, 1; PID:q483845
A:Note: The authors translated the codon AGT for residue 25 as Met
A:Genetics: 11/3; 48/3; 66/3; 114/3; 161/1; 222/3
A:Inserts:

```

Query Match 62.9% Score 76.5 DH 2 Length 235
Best Local Similarity 70.3% Prod. No. 7.8e-5.1
Matches 163 Conservative 17 Mismatches 43 Indels 9 Gaps 4

CY 1 MIVLAAPASPNSSILLLLLLSPCLRGTPDCCFSSTSTSSPFKKFRLTHLLKDYEV 60
CH 1 MIVLAAPASPP- TTYLLLLLLLSGSGSGGQSPFQSHSPSSSPFAVK IREI SYLLDLDYEV 59
CY 61 VAVNLQDRHCKALMSLEFLAQRWIEQLKTVAGSKMOTLLFVNTEIHFTVSCGFQPIRE 120
DB 60 VASNIQDEELCGILRLVLAORMHREKRTVAGSKMKGILLFVNTEIHFTVCAGQPPSC 119
CY 121 LRFVQTN-SHLKPCQTQLLALPKPCIGKACQNFNSKRLCEVQCGPSSSTLAPRSPFALEAT 180
DB 120 LRFVQTNISKRILQGESBEDVAKFWITR--QNSRSLLELQCGPSSSTLAPRMSRPIEAT 177
CY 181 FLPEPRQQLLLLLLLPLLVLLAAMGLRWQYARRK---GELAGVPLP 228
DB 178 APTAQPP-LLLLPLLVGQLLLAAMGICIMQWRKRTKRTFRGQGVPPVPS 227

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:44:07 : Search time 13.8798 Seconds

(without alignments)
782.659 Million cell updates/sec

Title: US-09-448-378-2
Perfect score: 1223
Sequence: 1 MVLAPAWMSNLSLLLL.....WQARRRGELHPGVPPLPSHP 211

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1212.5	99.1	232	1	FLJL_MOUSE
2	768.5	62.8	235	1	FLJL_HUMAN
3	95.5	7.8	909	1	RPS2_ARATH
4	89.5	7.3	941	1	GRR2_HUMAN
5	89	7.3	815	1	AD15_MOUSE
6	87	7.1	816	1	AD15_MOUSE
7	85	7.0	4513	1	AD15_MOUSE
8	84.5	6.9	1205	1	AT53_HUMAN
9	84	6.9	1409	1	AT53_HUMAN
10	83.5	6.8	552	1	CEFL_MOUSE
11	83.5	6.8	2476	1	ZAN_MOUSE
12	82.5	6.7	378	1	ZAN_MOUSE
13	80.5	6.6	395	1	LEUK_RAT
14	80	6.5	2812	1	INT_MOUSE
15	80	6.5	2812	1	INT_MOUSE
16	79.5	6.5	534	1	ZAN_HUMAN
17	79	6.5	1101	1	VAAG_SCHPO
18	78.5	6.4	122	1	YK72_MOUSE
19	78.5	6.4	1208	1	RCO4_HUMAN
20	78.5	6.4	3068	1	POLG_PEMYC
21	78	6.4	224	1	CMF3_HUMAN
22	78	6.4	806	1	STFB_MYCE
23	78	6.4	908	1	YK61_YEAST
24	77.5	6.3	266	1	HB2D_MOUSE
25	77.5	6.3	940	1	GRR2_RAT
26	77.5	6.3	983	1	B3A4_HUMAN
27	76.5	6.3	222	1	YB95_METH
28	76.5	6.3	326	1	VS09_ROT1
29	76.5	6.3	379	1	CYB_MOUSE
30	75.5	6.3	650	1	TNP2_MOUSE
31	75.5	6.3	1296	1	ASAL_ENTFA
32	76.5	6.3	3660	1	DMD_CHICK
33	76	6.2	438	1	PRL1_MOUSE

ALIGNMENTS

34	76	6.2	577	1	EP42_MOUSE
35	75.5	6.2	379	1	CYB_CAMDR
36	75.5	6.2	379	1	CYB_EULIM
37	75.5	6.2	379	1	CYB_MOUSE
38	75.5	6.2	379	1	CYB_MOUSE
39	75.5	6.2	379	1	CYB_MOUSE
40	75	6.1	433	1	ENOA_MOUSE
41	75	6.1	433	1	ENOA_MOUSE
42	75	6.1	602	1	YKOH_SCHPO
43	75	6.1	653	1	CANA_MOUSE
44	75	6.1	732	1	KEUL_HUMAN
45	75	6.1	758	1	VKQC_HUMAN

AC	FLJL_MOUSE	STANDARD	PRT	232 AA
AD	P49772: G54085			
DI	01-OCT-1996 (rel. 34, last sequence update)			
DI	01-OCT-1996 (rel. 42, last annotation update)			
DI	15-SEP-2003 (rel. 42, last annotation update)			
DE	St cytochrome precursor (Pms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3l)			
DE	Flt3l (Flt3l)			
DE	Flt3l (Flt3l)			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI-TaxID:10090			
FX	SEQUENCE FROM N.A.			
FX	MDLINP-94195428: PubMed-8145851			
RA	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Razaan J.F., Kastelein R., Budak S., Wager S., Shanley A., Dada G., Martini N., Peterson D., Menon S., Shandley A., Kuehnik M., Kuehnik G., Nankawa R., Remick D., Romcardo M.G., Zlotnik A., Rosner O., Dubreuil P., Birbaumer D., Lee F., Ligand for FLT3/PLK2 receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAs.			
RT	Nature 368:643-648(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RP	STRAN-SULC/			
RP	MDLINP-94084791: PubMed-7505204			
RA	Lyman S.D., James L., Vandenbos T., Davies P., Biessel K., Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J., Spiller R.R., Fletcher F.A., Markovitsky E., Farrar J., Foxworth D., Williams D.E., Beckmann M.P., Molecular cloning of a ligand for the FLT3/PLK-2 tyrosine kinase receptor: a proliferative factor for primitive hematopoietic cells.			
RI	Cell 75:1157-1167(1993).			
RJ	[3]			
RP	SEQUENCE FROM N.A.			
RP	MDLINP-96032581: PubMed-7566977			
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S., Structural analysis of human and murine flt3 ligand genomic loci.			
RI	Oncogene 11:1165-1172(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	MDLINP-95124710: PubMed-7824267			
RA	Lyman S.D., James L., Escobar S., Downey H., de Vries P., Biessel K., Stocking K., Beckmann M.P., Copeland N.G., Cleveland L.S., Identification of soluble and membrane-bound isoforms of the murine flt3 ligand generated by alternative splicing of mRNAs.			
RI	Oncogene 10:145-157(1995).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RP	MDLINP-95124710: PubMed-7824267			
RA	McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimaraes M.J.,			

```

RA Mattedi M.G., Rosnet O., Birbaumd D., Hannum C.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC
CC -1- SUBUNIT: Homodimer (soluble isoform) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Two soluble
CC isoforms are also produced by alternative splicing. One of which,
CC isoform 3/E6, is biologically active, while the other, isoform
CC 4/E6delta16, is inactive.
CC
CC -1- ALTERNATIVE PRODUCTS:
CC Event: Alternative splicing; Named isoforms=4:
CC Name=1: Synonyms=6C;
CC IsoId=P49772-1; Sequence=Displayed;
CC Name=2: Synonyms=5H;
CC IsoId=P49772-2; Sequence=VSP_004253;
CC Name=3: Synonyms=E6;
CC IsoId=P49772-3; Sequence=VSP_004254, VSP_004255;
CC Name=4: Synonyms=E6delta16;
CC IsoId=P49772-4; Sequence=VSP_004256;
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/isb.ch).
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: U04807; AAA18000.1; -
CC EMBL: L23636; AAA39436.1; -
CC EMBL: U29875; AAA90951.1; -
CC EMBL: U29875; AAA90952.1; -
CC EMBL: S76459; AAB33069.1; -
CC EMBL: S76461; AAB33070.1; -
CC EMBL: S76464; AAB33071.1; -
CC EMBL: U44024; AAA93306.1; -
CC EMBL: U44024; AAA93306.1; -
CC PIR: A49265; A49265.
CC
CC MGD: MGI:95560; Flt3l.
CC
CC DR Interpro: IPR004213; Flt3l_1lg.
CC Pfam: PF02947; flt3_1lg.1.
CC
CC KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
CC
CC FT SIGNAL 1 26
CC FT CHAIN 27 232
CC FT DOMAIN 27 189
CC FT TRANSMEM 190 2.0
CC FT DOMAIN 211 232
CC FT DISULFID 31 112
CC FT DISULFID 71 156
CC FT DISULFID 120 161
CC FT CARBOHYD 127 127
CC FT CARBOHYD 152 152
CC FT VARSPLIC 164 232
CC
CC FT VARSPLIC 164 169
CC FT VARSPLIC 170 232
CC FT VARSPLIC 159 163
CC
CC FT CONFLICT 141 141
CC FT CONFLICT 198 198
CC FT SEQUENCE 232 AA; 26141 MW; 3A3680D3C8H695BA6 CRC64;
CC
CC Query Match 99.1%; Score 1212.5; DB: Z; Length 232;
CC Best Local Similarity 99.6%; Pred. No. 6; 7e-99;
CC Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

01	MYLAPAMSPNSLLILLILLLSPCLRTSPCYSHSPISNSNKVFFRELTHLKLDP	
02	1 MYLAPAMSPNSLLILLILLLSPCLRTSPCYSHSPISNSNKVFFRELTHLKLDP	
03	61 VAVNIQDEKCKALMSLFLAQMWIEDQIKTIVAGSKMOTILEVNTIEHFVTSCTFQPLPE	
04	61 VAVNIQDEKCKALMSLFLAQMWIEDQIKTIVAGSKMOTILEVNTIEHFVTSCTFQPLPE	
05	121 LRFVQINISHLKTQCTQLLAKFCICKACQNSRLELVCCSPSSITLLPSPRTALEA	
06	121 LRFVQINISHLKTQCTQLLAKFCICKACQNSRLELVCCSPSSITLLPSPRTALEA	
07	121 ELPEPFRQLLLILLILPLTFVLAAMQIFRQARRRGELHPCVPLPSHP 231	
08	121 ELPEPFRQLLLILLILPLTFVLAAMQIFRQARRRGELHPCVPLPSHP 231	
09	121 ELPEPFRQLLLILLILPLTFVLAAMQIFRQARRRGELHPCVPLPSHP 232	
10	121 ELPEPFRQLLLILLILPLTFVLAAMQIFRQARRRGELHPCVPLPSHP 232	
11	RESULT 2	
12	FL3L HUMAN	
13	FL3L HUMAN	
14	FL3L HUMAN	
15	FL3L HUMAN	
16	FL3L HUMAN	
17	FL3L HUMAN	
18	FL3L HUMAN	
19	FL3L HUMAN	
20	FL3L HUMAN	
21	FL3L HUMAN	
22	FL3L HUMAN	
23	FL3L HUMAN	
24	FL3L HUMAN	
25	FL3L HUMAN	
26	FL3L HUMAN	
27	FL3L HUMAN	
28	FL3L HUMAN	
29	FL3L HUMAN	
30	FL3L HUMAN	
31	FL3L HUMAN	
32	FL3L HUMAN	
33	FL3L HUMAN	
34	FL3L HUMAN	
35	FL3L HUMAN	
36	FL3L HUMAN	
37	FL3L HUMAN	
38	FL3L HUMAN	
39	FL3L HUMAN	
40	FL3L HUMAN	
41	FL3L HUMAN	
42	FL3L HUMAN	
43	FL3L HUMAN	
44	FL3L HUMAN	
45	FL3L HUMAN	
46	FL3L HUMAN	
47	FL3L HUMAN	
48	FL3L HUMAN	
49	FL3L HUMAN	
50	FL3L HUMAN	
51	FL3L HUMAN	
52	FL3L HUMAN	
53	FL3L HUMAN	
54	FL3L HUMAN	
55	FL3L HUMAN	
56	FL3L HUMAN	
57	FL3L HUMAN	
58	FL3L HUMAN	
59	FL3L HUMAN	
60	FL3L HUMAN	
61	FL3L HUMAN	
62	FL3L HUMAN	
63	FL3L HUMAN	
64	FL3L HUMAN	
65	FL3L HUMAN	
66	FL3L HUMAN	
67	FL3L HUMAN	
68	FL3L HUMAN	
69	FL3L HUMAN	
70	FL3L HUMAN	
71	FL3L HUMAN	
72	FL3L HUMAN	
73	FL3L HUMAN	
74	FL3L HUMAN	
75	FL3L HUMAN	
76	FL3L HUMAN	
77	FL3L HUMAN	
78	FL3L HUMAN	
79	FL3L HUMAN	
80	FL3L HUMAN	
81	FL3L HUMAN	
82	FL3L HUMAN	
83	FL3L HUMAN	
84	FL3L HUMAN	
85	FL3L HUMAN	
86	FL3L HUMAN	
87	FL3L HUMAN	
88	FL3L HUMAN	
89	FL3L HUMAN	
90	FL3L HUMAN	
91	FL3L HUMAN	
92	FL3L HUMAN	
93	FL3L HUMAN	
94	FL3L HUMAN	
95	FL3L HUMAN	
96	FL3L HUMAN	
97	FL3L HUMAN	
98	FL3L HUMAN	
99	FL3L HUMAN	
100	FL3L HUMAN	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2003, 15:45:12 ; Search time 61.4678 Seconds
(without alignments)
969.778 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MVLAPAWSPNSLLLLLLL.....MORARRGELHPGVDLPSPHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriaph: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	71.9	172	11	061104 mus musculu
2	842.5	68.9	169	11	08VCH4 mus musculu
3	779.5	63.7	292	6	09GKE0 bos taurus
4	774.5	63.3	292	6	08MNM1 O8MNM1 bos taurus
5	774	63.3	294	6	09MZY0 O9MZY0 canis faml
6	761	62.2	291	6	09MKU9 O9MKU9 felis silve
7	678.5	55.5	274	6	09GKD9 O9GKD9 bos taurus
8	97.5	8.0	309	10	08LXZ9 O8LXZ9 arabidopsi
9	96.5	7.9	318	11	08CFN3 O8CFN3 mus musculu
10	95.5	7.8	909	10	08L5B3 O8L5B3 arabidopsi
11	95.5	7.8	909	10	08L101 O8L101 arabidopsi
12	95.5	7.8	909	10	042484 O42484 arabidopsi
13	94	7.7	355	4	09H665 O9H665 homo sapien
14	93.5	7.6	510	6	09BGY6 O9BGY6 macaca fasc
15	93.5	7.6	909	10	08L3R0 O8L3R0 arabidopsi
16	93.5	7.6	909	10	08L4Y0 O8L4Y0 arabidopsi

17	93.5	7.6	909	10	08L100	08L100 arabidopsi
18	93.5	7.6	909	10	08L4X9	08L4X9 arabidopsi
19	93.5	7.6	909	10	08L587	08L587 arabidopsi
20	90.5	7.4	909	10	08L3M3	08L3M3 arabidopsi
21	90.5	7.4	909	10	09ASP5	09ASP5 arabidopsi
22	89	7.3	340	6	08H290	08H290 saginus oe
23	89	7.3	864	11	08C720	08C720 mus musculu
24	88.5	7.2	326	12	083443	083443 murine rota
25	88.5	7.2	326	12	083448	083448 murine rota
26	88.5	7.2	493	11	08BR09	08BR09 mus musculu
27	88.5	7.2	513	11	08JZU3	08JZU3 mus musculu
28	88.5	7.2	905	10	08LXZ8	08LXZ8 arabidopsi
29	88	7.2	258	4	09H563	09H563 homo sapien
30	88	7.2	765	4	094824	094824 homo sapien
31	88	7.2	843	4	014584	014584 homo sapien
32	88	7.2	1028	5	08SXA6	08SXA6 drosophila
33	88	7.2	1254	5	09VFS1	09VFS1 drosophila
34	87.5	7.2	477	11	09CYB2	09CYB2 mus musculu
35	87.5	7.2	1231	10	09KXZ2	09KXZ2 arabidopsi
36	87	7.1	291	16	09ZH99	09ZH99 yerisina pe
37	87	7.1	809	11	08CAB2	08CAB2 mus musculu
38	87	7.1	1256	5	09VFS0	09VFS0 drosophila
39	86.5	7.1	2111	5	091802	091802 drosophila
40	86.5	7.1	4167	5	09GPN8	09GPN8 drosophila
41	86	7.0	962	5	096164	096164 plasmodium
42	85	7.0	181	5	017726	017726 caenorhabdi
43	85	7.0	1305	2	066521	066521 enterococcu
44	85	7.0	4513	10	09MBF8	09MBF8 chlamydomon
45	84.5	6.9	364	4	056AY5	056AY5 homo sapien

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	172 AA.
Q61104			
AC	Q61104:		
D1	01-NOV-1996 (TREMBLrel. 01, Created)		
D7	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
D1	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Flt3 ligand, T169 form.		
CN	Flt3L.		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OT	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Jacson K.,		
RA	Mattson J., Tsai S., Luh J., Guimaraes M., Mattei M.-G., Rosnet C.,		
FA	Birbaumer D., Hannum C.,		
RT	"Flt3 ligand: expression, genomic organization, alternatively spliced		
RT	forms and processing."		
RL	Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.		
DR	EMBL: U44024; AA93305.1; -		
DR	HSSP: P49771; IETF.		
DR	MCD: MG1:95560; F1C31.		
DR	InterPro: IPR004213; Flt3_lig.		
DR	Pfam: PF02947; flt3_lig. 1.		
SO	SEQUENCE 172 AA; 19465 MW; 04FOA01071E3384 CRC64;		
Query Match	71.9%;	Score 879;	DB 11;
Best Local Similarity	98.2%;	Pred. No. 1.2e+81;	Length 172;
Matches 165;	Conservative 1;	Mismatches 2;	Indels 0;
DB	1 MVLAPAWSPNSLLLLLLLSPCLRGFPDYSHPISSNKVFRELTDLKDYVT 60		
DB	1 MVLAPAWSPNSLLLLLLLSPCLRGFPDYSHPISSNKVFRELTDLKDYVT 60		
QY	1 VAVNIODEKHCXALSLFLAQMIEQLTVAASKMOTLELVNTEIHVFISCTQPLDEC 120		
QY	1 VAVNIODEKHCXALSLFLAQMIEQLTVAASKMOTLELVNTEIHVFISCTQPLDEC 120		
DB	61 VAVNIODEKHCXALSLFLAQMIEQLTVAASKMOTLELVNTEIHVFISCTQPLDEC 120		
DB	61 VAVNIODEKHCXALSLFLAQMIEQLTVAASKMOTLELVNTEIHVFISCTQPLDEC 120		

```

OY 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTL 168
Db 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTL 168

RESULT 2
OYCH4 10 OYCH4 PRELIMINARY: PRT: 169 AA.
AC OYCH4:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Similar to FMS-like tyrosine kinase 3 ligand.
GN FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
PC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019801; AAI19801.1; -.
DR MGD: MGI:95560; Flt3l.
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig.1.
KW Kinase.
SQ SEQUENCE 169 AA: 18986 MW: 584CA47D9724EFPZ CRC64:

Query Match 68.9%; Score 842.5; DB 11: Length 169;
Best Local Similarity 92.5%; Pred. No. 6e-78;
Matches 161; Conservative 0; Mismatches 4; Indels 9; Gaps 1;

OY 1 MTVLAPAMSPNSLLILLLISPCLRGPPDCYFSSHPSSNFKYKFEITDHLKDYPT 63
Db 1 MTVLAPAMSPNSLLILLLISPCLRGPPDCYFSSHPSSNFKYKFEITDHLKDYPT 63
OY 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120
Db 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120
OY 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSP 174
Db 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSP 174
OY 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSP 165
Db 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSP 165

RESULT 3
OYCH4 10 OYCH4 PRELIMINARY: PRT: 292 AA.
AC OYCH4:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE FLT3 ligand isoform-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
PC MEDLINE=20570936; PubMed=11120823;
RA Mwangi W., Brown W.C., Palmer G.H.;
RL *Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain;
RT required for receptor binding and function using naturally occurring
KT ligand isoforms.
J. Immunol. 165:6966-6974(2000).
DR EMBL: AF282985; AAF93322.1; -.
DR HSSP: P49771; IETE.
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig.1.

```

```

SQ SEQUENCE 292 AA: 32390 MW: D68B9ED79221202D CRC64:

Query Match 63.7%; Score 779.5; DB 6: Length 292;
Best Local Similarity 63.2%; Pred. No. 3e-71;
Matches 164; Conservative 20; Mismatches 43; Indels 33; Gaps 5;

OY 1 MTVLAPAMSPNSLLILLLISPCLRGPPDCYFSSHPSSNFKYKFEITDHLKDYPT 60
Db 1 MTVLAPAMSPNSLLILLLISPCLRGPPDCYFSSHPSSNFKYKFEITDHLKDYPT 60
OY 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120
Db 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120
OY 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSPALCAT 178
Db 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSPALCAT 178
OY 181 ELPEPR-PROQLDILLLPLTLVLAAMGL-RMGRARRR----- 218
Db 179 SLPGQSPILLILLLILPLVALLLATAMGLRMGRARRRTRYPGERRRRLRRPSSILPA 238
OY 219 -----GELHPGVPLPSHP 231
Db 239 -----GELHPGVPLPSHP 231

RESULT 4
OYCH4 10 OYCH4 PRELIMINARY: PRT: 292 AA.
AC OYCH4:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE FLT3 ligand.
GN FLT3 LIGAND.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
PC Cloning of a cDNA for bovine flt3 ligand.
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB05-841; BAB79634.1; -.
DR InterPro: IPR004213; Flt3_lig.
DR Pfam: PF02947; flt3_lig.1.
KW Kinase.
SQ SEQUENCE 292 AA: 32388 MW: 2A797E0C1199C1D9 CRC64:

Query Match 63.3%; Score 774.5; DB 6: Length 292;
Best Local Similarity 62.8%; Pred. No. 9.6e-71;
Matches 164; Conservative 20; Mismatches 44; Indels 33; Gaps 5;

OY 1 MTVLAPAMSPNSLLILLLISPCLRGPPDCYFSSHPSSNFKYKFEITDHLKDYPT 60
Db 1 MTVLAPAMSPNSLLILLLISPCLRGPPDCYFSSHPSSNFKYKFEITDHLKDYPT 60
OY 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120
Db 61 VAVNIODEKHCKALMSLFLAORWIEQLKTVAAGSKMOTLLEDVNTIEHFVTSCTFQPLPFC 120
OY 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSPALCAT 180
Db 121 LRFVOTNISHLLKDTCTOLLAIKPCIGKACONFSRCLEVOCCPDSSTLPRSPALCAT 178
OY 181 ELPEPR-PROQLDILLLPLTLVLAAMGL-RMGRARRR----- 218
Db 179 SLPGQSPILLILLLILPLVALLLATAMGLRMGRARRRTRYPGERRRRLRRPSSILPA 238
OY 219 -----GELHPGVPLPSHP 231
Db 239 -----GELHPGVPLPSHP 231

```